Mon Jun 26 09:10:26 2000

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AS2460 Sequence 4
AR009152 Sequence
M73260 Msstadenovi
701917 Adenovirus
582508 9E4: Orf2.
AF108105 Human aden
X51800 Adenovirus
119443 Human aden
AD3481 Adenovirus
119443 Human aden
AD36117 Porcine a
177082 Canine aden
V07760 Canine aden
V07760 Canine aden
V07760 Canine aden
V07760 Canine aden
AF030154 Bowine aden
AF030154 Homo sapi
AC016797 Homo sapi
AC01638 Homo sapi
AC01638 Homo sapi
AC01588 Homo sapi
AC01589 Homo sapi
AC01294 Measles vir
X1656 Measles vir
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X1656 Measles vir
X1656 Measles vir
AB012949 Measles v
AB012949 Measles v
AC016946 Homo sapi
                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AL135905
AC006760
AC006760
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MEAMIBE
AB012948
AB012948
AC016946
AC010746
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AR009152
ADRCOMPGEN
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882508
AT12CGA
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ADRESNOME
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CAU77082
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AC016797
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AC016343
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AF083334
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184762
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149093
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3.9 2041
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.8 309026
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6447...
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583...
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35.2
35.2
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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(IN MAStademovirus h5 gene, complete genome.)

(M M73260 M29978

(M M73260 L GI:209842

(M M3260 L GI:209842
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1. 35935
7. Organism-Human adenovirus type
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Celma,M.L., Pan,J. and Weissman,S.M.
Studies of low molecular weight RNA from cells infected adenovirus 2. I. The sequences at the 3' end of VA-RNA I 78046048
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Studies of low molecular weight RNA from cells infected adenovirus 2. II. Heterogeneity at the 5' end of VA-RNA
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Jornvall, H., Ohlsson, H. and Philipson, L.
An acctylated N-terminus of adenovirus type 2 hexon p.
Blochem. Blochys. Res. Commun. 56 (2), 304-310 (1974)
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Pan, J., Celma, M.L. and Weissman, S.M.
Studles of low molecular weight RNA from cells adenovirus 2. III. The sequence of the promoter J. Biol. Chem. 252 (24), 9047-9054 (1977)
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Obe, K. and Weissman, S.M.
The noclotide sequence of a low molecular from cells infected with adenovirus 2
J. Biol. Chem. 246 (22), 6991-7009 (1971)
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Ziff,E.B. and Evans,R.M.
Coincidence of the promoter and capped 5' tadenovirus 2 major late transcription unit
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Zain,B.S. and Roberts,R.J.
Characterization and sequence analysis
the hybrid virus Ad2+ND
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J. Mol. Biol. 128 (4), 577-594 (1979)
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Sequence analysis of adenovirus DNA.
carboxy-terminal end of the gene for virology 91 (2), 477-480 (1978)
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Arrand, J.R. and Roberts, R.J.
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Precise localization and nucleotide sequence of the two mouse
mitochondrial rRNA genes and three immediately adjacent novel
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Nucleic Acids Res. 9 (1), 1-17 (1981)
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Buttner,W. and Veres-Molnar,Z.
Butcatization of the 3'-terminal end of the
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FEBS Lett. 122 (2), 317-321 (1980)
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Shinagawa.M., Padmanabhan,R.V. and Padmanabhan,R.
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The uncleotide sequence of the right-hand terminal Smal-K fragment of adenovirus type 2 DNA
Gene 9 (1-2), 99-114 (1980)
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Sequence analysis of adenovirus DNA. IV. The genomic sequences
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Gallbert, F., Herisse, J. and Courtols, G.
Nucleotide sequence of the EcoRI-F fragment of adenovirus
Gene 6 (1), 1-22 (1979)
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                                                                                                                                                                                                                      Shingawa, M. and Padmanabhan, R. Nucleotides sequence at the inverted terminal repetition adenovirus type 2 DNA adenovirus type 2 DNA Blochem. Biophys. Res. Commun. 87 (3), 671-678 (1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                       messenger RNA
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Zain,B.S. and Roberts,R.J.
Sequences from the beginning of the fiber
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Herisse, J., Courtois, G. and Gallbert, F
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30029717
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                            copy of adenovirus 2 fiber mRNA
Cell 16 (4), 851-861 (1979)
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80155185
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79211248
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/word="This sequence comes from Fig. 1"
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/brotein_id="AaB37506_1"
/db_rsf="G1:1699393"
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PLOMENDEIDGGPAFNYLLMLDVRVEFDLEATVEHLENRVGFDLAVCFHQHSGGERL
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1278. .1631
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REMYMGSVFMRGRHLIYCERWYDGHVGSIIPNMSFGWSALNYGLLNNWYIMCCTYCE
NMAEIRMRCCARRTRRIMLKAVGIIVRETCDPDPICSSRTEPRRGRLLRALMERHRPI
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ENISLERATRAERTYTVTVKWAGGGRLTTRAGVKINKDT"

701 c 848 g 811 t
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37.2%; Score 328.8; DB 16; Length 3119;
Best Local Similarity 63.1%; Pred. No. 9.3e-85;
Matches 526; Conservative 0; Mismatches 302; Indels 6;
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/note="This sequence comes from Fig.
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/note="This sequence comes fx
/codon_start=1
/protein_id="AAB37506.1"
                                                                                                                                      889. .1281
/gene="orf2"
/note="This sequence comes
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/codon_start=1
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/protein_id="AAB37505.1"
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/protein_id="AAB37508.1"
/db_xref="G1:1699395"
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2798. .3046
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889. .1281
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/gene="orf4"
1634. .1996
/gene="orf4"
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/gene="orf6"
1926. .2804
/gene="orf6"
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Human adenovirus type 9

Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

1 (bases 1 to 3119)

Javier, R. and Shenk, T.
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$82508.1 GI:1699390
                 protein; This sequence comes from
                                                                              33597 TACCGGGAGGTGAATTACAACATGCCAAAAGGGTAATGTTATGTCCAGCGTGTTT 33538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammary tumors induced by human adenovirus type 9: a role for viral early region 4 gene
Breast Cancer Res. Treat. 39 (1), 57-67 (1996)
ctgtgttgtgccaacattgatatcatgacgagcatgatgatccatggttacgagtcctgg
                                                             getetecactgteattgttecagteceggttecetgeagtgtatagecegegggeaggtt
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1. 3119
/organism="Human adenovirus type 9"
/db_xref="taxon:10527"
471. .848
/gene="E4"
/gene="E4"
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/gene="E4"
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I (bases; dsDNA viruses; no RNA stage; Adenoviridae; Mastadenovirus.

I (bases I to 35100)

Chillon,M., Bosch,A., Zabner,J., Law,L., Armentano,D., Welsh,M.J. and Davidson,B.L.

Group D adenoviruses infect primary central nervous system cells more efficiently than those from group C

J. Virol. 73 (3), 2537-2540 (1999)
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             1941 CAATCCAGCTCGCTCGCCATCATCGCAGGGCCCGTTTACCACGATCTGATGAG 2000
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Muman adenovirus type 17 complete genome.
AF108105
AF108105.1 GI:4416335
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XNSTNVQSNLDRLYTDVREAVAQRERFKNEGLGSLVALNAFLATQPANVPRGQDDYIN
FISALRLMYTEVPQSEVYQSGPDYFEQTSRGGLQTVNLSQARKNLRGLMGVQAPVGDR
STVSSLLTPNSRLLLLIAPFTDSGSVNRNSYLGHLLTYREAIGQAQVDEQTFQEIT
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GHRLMETRGKKRIKKRIGGKLVPDPEQPELTWLVECETVCAHCGADAFAPESVFLAPKL
YALQSLLCPACGRSSKGKLRAKGHAAEALNYELMVNCYLADAQGEDRARFSTSRMSLK
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EMP"
2 (bases 1 to 35100)
Armentano,D. PhD and Souza,D.W.
Direct Submission
Submitted Discoular Biology, Genzyme Corporation, 31
New York Ave., Framinham, MA 01701-9322, USA
Location/Qualifiers
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/db_xref="taxon:4692"
complement(4991. .8266)
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/protein_id="AAD20326.1"
/db_xref="GI:4416342"
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/db_xref="GI:4416337"
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complete genome; core protein; DNA polymerase; DNA-binding protein; endoprotease; fiber protein; hexon protein; large T-antigen; maturation protein; minor core protein; penton protein; peripentonal hexon-associated protein; promoter; repeat region; small t-antigen; transcriptional activation.

Human adenovirus type 12

Human adenovirus type 12

Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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                                                                                                                                                                                                                     ggttacgagtcctgggctctccactgtcattgttccagtcccggttccctgcagtgtata
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ATPSAALDMTARNMEPSMYAANRPFINKLMDYLHRAASMNSDYFTNAILNPHWLPPPG
FYTGEYDMPDPNDGFLWDDVDSAVFSPTLQKRQEAVRTPASEGAVGRSPFPSLGSLHS
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REPAPAPRROKHDRORGLVWDDEDSADDSSVLDLGGSGGVNPISKILQPKLGRRMF"
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SPQVLPTLRRNQEELYRFLARHSPYFRSHRAAIEHATAFDKNKQLRVSQ"
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/db_xref="G1:4416341"
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SANKLSLKVGHGLKILDDKSAGGLKDLIGKLVVLTGKGIGTENLQNTDGSSRGIGISV
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SEAYKNAVEFMPNLVAYPKPTJGSKKYARDIVYGNIYLGGLAYQPVVIKVTFNEEADS
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9877 c 9981 g 7250 t
                                                                                                                                                                                                             /product-"penton base"
/protein_id-"AAD20322.1"
                                                                                                                                                                                                                                                                                                 'db_xref-"GI:4416338
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DVARGEGGGAEPCGGGEVNMEDQYOEGHYLDSGEGPSCADDRDKQEKKESLKEAAVLS
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AKLALRPDCSYRITKTVTITSCAYIIGNGAIVEVDTSDRVAFRCRMGGMGPGYVGLDG
ITFINVRFAGDKFKGIMFEANTCLVLHGVYFLNFSNICVESNNKVSARGCTFYGCWKG
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ydloyesagednnegayneffpeslilaaseglflpeppylspygepfgecmpglhp
edmollcyemgfpcsdsedegdengmahysasaaaaaadrereefqudhpelpghnck
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Edyreefentladcpgllasidlcyhlyfoekvyrsidfssygrivasiaflatidk
Wsekshlswdymldymsmqlwrawlkrryciyslarplimpplptlqeekeeennpav
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/note="crossref Ad12 EPD07152"
/function="Elb promoter region (-499 to +100)"
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'note="crossref SWISS-PROT:EIBL_ADE12, P04491"
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/note="crossref SWISS-PROT:E1BS_ADE12, P04492"
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/protein_id="CAA51878.1"
/db_xref="GI:313363"
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                                                                                                                                          l. .161
/function="inverted terminal repeat"
                                                              /organism="Human adenovirus type
/db_xref="taxon:28282"
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Sapporo Igaku Zashi 52, 253-267 (1983)
10 (bases 20966 to 22966)
110 (bases 20966 to 22966)
121 (bases 20066 to 22966)
132 Structure and schalk, P.M., Speljer, J.G. and Sussenbach, J.S.
Structure and function of adenovirus DNA binding protein:
comparison of the amino acid sequences of the Ad5 and Ad12 proteins derived from the nucleotide sequence of the corresponding genes
Virology 128 (1), 140-153 (1983)
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Juttermann,R., Weyer,U. and Doerfler,W.

Juttermann,R., Weyer,U. and Doerfler,W.

Juttermann,R., Weyer, W.

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Engler,J.A. and van Bree,M.P.
Engler,J.A. and van Bree,M.P.
Arb nucleotide sequence of the gene encoding protein IVa2 in human
adenovirus type 7
Gene 19 (1), 71-80 (1982)
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Shinagawa, M. and Padmanabhan, R.
Shinagawa, M. and Padmanabhan, R.
Comparative sequence analysis of the inverted terminal repetitions from different adenoviruses
Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3831-3835 (1980)
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Shibata, H., Zheng, J. H., Koikeda, S., Masamune, Y. and Nakanishi, Y.
Cis- and trans-acting factors for transcription of the adenovirus
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Kimura,T., Sawada,Y., Shinawawa,M., Shimizu,Y., Shiroki,K., Shimojo,H., Sugisaki,H., Takanami,M., Uemizu,Y. and Fujinaga,K. Nucleotide sequence of the transforming early region Elb of adenovirus type 12 DNA: structure and gene organization, and comparison with those of adenovirus type 5 DNA
Nucleic Acids Res. 9 (23), 6571-6589 (1981)
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Tolun, A., Alestrom, P. and Pettersson, U.
Sequence of inverted terminal repetitions from different
adenoviruses: demonstration of conserved sequences and homology
between SA7 termini and SV40 DNA

Coll 17 (3), 705-713 (1979)
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Nucleotide sequence of the genes encoded in early region 2b of human adenovirus type 12
Gene 46 (2-3), 187-195 (1986)
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                                                                                                                                                                                                                                        5 (bases 1 to 3957)
van Ormondt, H. and Gallbert, F.
Nucleotide sequences of adenovirus DNAs
(Gurr Top. Microbiol. Immunol. 110, 73-142 (1984)
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/protein_id="CAA51880.1"
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                                 LVGRPRSKLSVKKCLFEKCVLALIVEGDAHIRHNAASENACFVLLKGNAILKHNNVCG
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QCNFSHSNIMLEPEYFSRVCLNGVFDLSVELCKVIRINDDTRHRCRQCECGSSHLELR
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                                                                                                                                                                                 3374, .3808
/note="crossref SWISS-PROT:HEX9_ADE12,
                                                                                                                                                                           'replace="atactgaat"
                                                                           2071. .2073
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2417. .2418
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                                                                                                                                                                                                         codon_start-1
                                                                                                                                                   2479. .274]
/citation=[9]
                                                                                                                                       /replace="ga
2479. .2741
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The complete (06-FEB-1990) Hogenkamp T., Institute of Molecular 10.10043) for overlapping sequence.

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Corporation="Human adenovirus type 12"

Strain="Human adenovirus type 12"

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Forduct="early E4 34 KD protein"

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Human adenovirus type 12.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
1 (bases 1 to 3498).
1 (bases 1 to 3498).
Nucleotide sequence of the right 10% of adenovirus type 12 DNA encoding the entire region E4.
Nucleotide sequence of the right 10% of adenovirus type 12 DNA encoding the entire region E4.
Nucleotide Acids Res 18 (10), 3065-3066 (1990).
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PEAFYILASLREWLYFAFLTERQRCKQKGRGAITSGRTWFCFFKYEDARKSVVYDAAR
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/db.xref="d:-6018360"
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OSGSIANTERFENDNAPALLIFIEIRAVALLEAVVEHLENRLQFDLAVIFHQHSGGDRCH
IEDDRAQIADBLD.
1 864 c 620 g 883 t
                                                                          31617 ccasacrecraristraaaastrerrcaasraarrecreaaaacacrerraa 31558
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Submitted (06-FEB-1990) Hogenkamp T., Institute of Molecular
Biology (Cancer Research), University of Essex, Hufelandstr 55,
4300 Essen 1, F R G
See <V000043> for overlapping sequence.
Location/Qualifiers
        caaggcgccttatgctgcgggcggtgcgaatcatcgctgaggagaccactgccatgttgt
                                                                                                                                                        785 attectgeaggaeggagggggggggggggggtttattegegegetgetgeageaceace
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Hogenkamp, T.
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DVEVDGFEEDANOEAVDGMFPERLLSEAESSAAESGGDSGVGEELLPVDLDLKCYEDG
LPPSDPETDBATEABEBAAMPTYVNBNBNELVLDCPBNPGRGCRACDFHRGTSGNPEA
MCALCYMRLTGHCIYSPISDAEGESEGGSPEDTDFPHPLTATPPHGIVRITPCRVSCR
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/translation="MRMLPDFFTGNWDDMFQGLLETEXVFDFTTLOWNFDFT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The genes encoding the DNA binding protein and the 23K protease of adenovirus types 40 and 41 virology 163, 1-10 (1988) 88160034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 (bases 1 to 34214)
Davison,A.J., Teliord,E.A., Wetson,M.S., McBride,K. and Mautner,V.
The DNA sequence of adenovirus type 40
The DNA sequence 234 (4), 1308-1316 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pieniazek, N.J., Slemenda, S.B., Pieniazek, D. and Luftig, R.B. VA RNA region of human enteric adenovirus type 40 shows homology the VA region of simian adenovirus type 7 upublished (1992) Location (Qualifiers
                                                                                                                            fastidious adenovirus types 40 and 41 Gene 58, 109-126 (1987)
                                                                                                                                                                                                                                                                                           Analysis of structure and function of human adenovirus type 40 leftmost 1.85 kb region including transforming ElA gene Sapporo Igaku Zasshi 57, 59-66 (1988)
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Toogood.C.I., Murall,R., Burnett,R.M. and Hay,R.T.
Troogood.C.I., Murall,R.) beach sequence, predicted structure
The adenovirus type 40 hexon: sequence, predicted structure
relationship to other adenovirus hexons
J. Gen. Virol. 70, 3203-3214 (1989)
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Vos, H.L., van der Lee, F.M., Reemst, A.M., van Loon, A.E. and Sussenbach, J.S.
                                                                                                          2 (sites)
van Loon, A.E., Ligtenberg, M., Reemst, A.M., Sussenbach, J.S.
Rozijn, T.H.
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Kildi,A.H. and Erasmus,M.J.
Sequence characterization of the adenovirus 40 fiber gene
Virology 172, 134-144 (1989)
89370295
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Nucleotide sequence of the adenovirus type 40 inverted repeat: Close relation to that of adenovirus type 5 Virology 156, 414-416 (1987)
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join(486. .669,1088. .1311)
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/standard_name="EIA 249R"
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/organism-"Human adenovirus
/isolates"Dugan:
/db_xref="taxon:28284"
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/note="for ElA"
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/product="E1A"
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Ishino, M.
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Human adenovirus type 40
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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                                                                                                                                                               1597 CTTCGGAAAAİTCTTİATGGCCTGAGTGTAATAGİCTĞACTTACATAATGTAAĞTGAĞĞ 1538
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Ishino,M., Sawada,Y., Yaegashi,T., Demura,M. and Fujinaga,K.
                                                                                                                       68 ctccgtacagtagggatcgtctacctccttttgagacagaaacccgcgctac---catac 124
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                                  Length 3498;
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Human adenovirus type 40, complete genome.
119443
                                     DB 16;
                                  Score 273.8; DB 16;
Pred. No. 8.9e-69;
0; Mismatches 322;
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                                          Query Match
Best Local Similarity 59.6%;
Matches 480; Conservative
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IPPSDPetdbateaeeraamtyvmeneruvlocpenpgrgcracpisdagesesg
SPEDTDFPHPLATPPHGIVRTIPCRVSCRRRPAVECIEDLLEDFTDEPLNLSILKRP
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join(486. .927,1088. .1311)
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Standard_name="EIA 249R"
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MRNA

exon

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exon

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<del>П.Т.Ц.</del>Т.,,,

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join(<533. .1043,1141. .1274)
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                                                                                                                          RPARTOEEVLL"
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boul.
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/note="possible promoter region of ElA genes"
533. .1222
/note="bescription: ElA; homologous to ElA 289R of human adenovirus 2 and 5; putative early genes transactivater, induction of host cells DNA synthesis and activate p53 dependent apoptosis cascade"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
1 (bases 1 to 34094)
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/note="porcine adenovirus 3 strain 6618 and adapted for cell
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                              32385 GGGTCTCTTCAATGTAAGGCGGGGGTGTAAGTGTTAGCAAATTGGTTTAAAATGATGTT 32326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               porcine adenovirus serotype 3, complete genome porcine adenovirus serotype 3, complete genome Unpublished (1999)

2 (bases 1 to 34094)

Larocque, ... Malenfant,F., Massie,B. and Dea,S.
Direct Submission Boby/EMBL/GenBank databases. Submitted (14-APR-1999) to the DDBJ/EMBL/GenBank databases. Larocque, INRS-Institut Armand-Frappier, Biotechnology; 531 larocque, INRS-Institut Armand-Frappier, Biotechnology; 531 (E-mailies, Laval, Quebec HIN 423, Canada (E-mailienie) Location/Qualifiers
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/note="TATA box of major late promoter (MLP)"
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region of terminal protein of human ad2 and ad5; the start
codon is not identified yet"
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1461. 2069
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putative inhibits apoptosis, (Bc1-2 homologue)"
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45.2%; Pred. No. 4.9e-08;
tive 0; Mismatches 380;
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RVEEAGGUSAARAHMSAASLAQAY EGTVREEVNFOKTFNNNVRTLYSRDEYTMGLMHL
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/gene="ElB"
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4085. .4090
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SAVAARVLSTAVEAVYEBPLAPPSPFVLDCPEVPGVNCRSCDYHRFHSKDFNLKCSLC
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/product-min 246786101.1."
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YRMAHAFNYGEVLL"
/poin(533...1043,1141...1274)
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Direct Submission
Direct Submission
Submitted (16.FEB-1999) Larocque D., INRS-Institut Armand-Frappier,
Submitted (16.FEB-1999) Larocque D., INRS-Institut Armand-Frappier,
Submitted (16.FEB-1999) Larocque D., INRS-Institut Armand-Frappier,
Sal boul. des Praities, Laval, Quebec H7N 423, Canada
Location/Qualiflers
1. 3409418m="Porcine adenovirus 3"
//strain="IAF"
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                                                                                                                                                                                                                                                                                                                                                                                                Porcine adenovirus 3
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
1 (bases 1 to 34094)
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/db_xref="high titer clone derived from strain 6618 and /note="high titer clone derived from strain 6618 and adapted for cell line PKA (pig kidney, porcine circovirus
                                                                                                                                                                                                               AJ237815
AJ237815.1 GI:4678602
AJ237815.1 GI:4678602
AJ237815.1 GI:4678602
IO kDa protein; D29; J4R; 229R; 474R; 52 kDa protein; COOH
region; DBP; EIB; EIB; fiber protein; hexon; IIIa; penton protein;
pIX; proteinase; PTP; pVII; pVIII.
Porcine adenovirus 3.
                                                                                                                                       PAD237815 34094 bp DNA VRL 04-MAY-1999
Porcine adenovirus serotype 3 complete genome, strain IAF.
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/gene="EIA"
1461. 2061
/function="putative inhibitor of apoptosis (Bcl-2
homologue)"
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/rpt_spype=INVERTED
/rpt_type=TERMINAL
449. .452
/gene="ElA"
/note="possible promoter region of ElA genes"
/gene="ElA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Larocque, D., Malenfant, F., Massle, B. and Dea, S. porcine adenovirus serotype 3, complete genome
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/codon_start=1
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/qene="E1A"
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                                                                                             RESULT 11
PAD237815/c
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TITLE
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                               ATVERGOESTIGELSALRILVSEVPOTEVERSCPHTFLQAARDGSKTVNILNOAMENILR
PHOGLOAPAGERGHVSSLITPNTRILLILVAPFAEEMNVSRSSTIGHLITLITERTLAN
LHVDERTYOETTSVRRALGDEDDAARLOATLISTTRRORMENDAAVELTAEERSTILRY
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RAQEMOLPVARFSRRHQPRROALEDDEEEEDWRODRFFFFEDAISSRLFTWRT
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STYDMAFPDDVLAPGCAIDTTFSRLNNLLGIRKRYPYQEGFRLTYBDLAGGNIPALL
DLTTVDGENSSTIKPLKOBDSKRSKYHVGEDPERGDTFTYRGWYLAYNGDPATGTAS
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VQRYIVTDARRNCPTVYRSLGVVTPFRVDLSSRTF"
MVYDALLERVSRYNSGNVQTNLDRLSQDVRQVIAQRERSSANNLGSLAALNAFIASLP
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AGTNATKDMFLVQMLAHYNIGYQGYHLPEGYRDRYSFYLRNFEDMCRQVPDYAHHKDE
TEVPFTYNGYRSGFYSAAFTAGMRECHPYPANWPYPLIGEDAVQTVTQRKFLCDRTL
HQPHRGVIEAVYLRTPFSAGNATT"
1930. .22544
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/function="major core protein; packaging of viral DNA"
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Pred. No. 4.9e-08;
0; Mismatches 380; Indels 6
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1906. 21912
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WATCHES 319, CONSERVAT
MATCHES 319, CONSERVA
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31751 AATCGCATCTTCTGGTGGTTCAGGGAGGCGGTGAACCTGCCCAGCGTGAGTCGGGGGAGG 31692
                                                         31868 ----GGCGCGCGAGCTGTGGAACTTTCATTGCCACTGTCTGAAAAGGTCCAGTCTGGAGGC 31812
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catggttacgagtcctgggctctccactgtcattgttccagtcccggttccctgcagtgt 402
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"Characterization of the early region 4 of porcine adenovirus type 3";
                                                                                                                                               403 atagcoggogggoaggttttggcoagctggtttaggatggtggtggatgcgcoatgttt
                                                                                                                                                                                                                                                                                                      aatcagaggtttatatggtaccgggaggtggtgaattacaacatgccaaaaggaggtaatg
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/organism="Porcine adenovirus 3"
/sub_strain="6618"
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04-JAN-1996 (Rel. 46, Last updated, Version 1)
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Reddy, P.S., Idamakanti, N., Derbyshire, J.B. and Nagy, E.
Characterization of the early region 4 of porcine adenovirus type 3
Virus Genes 15 (1), 87-90 (1997)
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Reddy, P.S., Idamakanti, N., Song, J.Y., Lee, J.B., Hyun, B.H.,
Raddy, P.S., Idamakanti, N., Bae, Y.T., Tikoo, S.K. and Babluk, L.A.
Bae, Y.T., Tikoo, S.K. and Babluk, L.A.
Nucleotide sequence and transcription map of porcine adenovirus
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                                         03-JAN-1999
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                                      VRL
Porcine adenovirus 3 strain 6618, complete genome.
AF083132 L43077 U10433 L43363
AF083132.1 GI:4092658
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13662. 15116
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/specific_host="Sus scrofa"
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Virology 212 (1), 237-239 (1995)
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                                                                                                                                                                                                                                       /note="homology to Human Adenovirus 34 kDa polypeptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2161 TACAGCCTGTGTGGGGGGTTGGAGCTGGAGCAGATATGTTTCAGCCCGGAGACGCTGTGC 2220
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SQ ...Sequence.3028 BP; 562 A; 789 C; 991 G; 686 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match.
Best Local Similarity 45.0%;
Matches 317; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2903. .2909
                                                                                                  . .327
                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyA_signal
                                                                                                        TATA_signal
TATA_signal
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LTAEGISLSGPGLSNSETGLSLOVTAPLOPGGNALTLPLAAGLORTDGGMGVKLGSG
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TTIPNGTFELCLTRVGGLYLGSFALKSSIDLTSMTKKVNFIFDGAGRLQSDSTYKGRF
GFRSNDSVIEPTAAGLSPAWLMPSTFIYPRNTSGSSLTSFVYINGTYVHVDIKVNTLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNGYSLEFNFONMSFSAPFSTSYGTFCYVPRRTTHRPRHGPFSLRERRHLFQLLQQ"
30205. .30929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31992 TIGGAGATIGIGGICCCCIGGCGCTACATTCCCATCATAGATTCCTGCAG 31933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31932 TACAGCCTGTGGGGGGTTGGAGCTGGAGAGAGATATGTTTCAGCCCGGAGAGGCTGTGC 31873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 acaatgcacaacgtgagttacgtgcgaggtcttccctgcagtgtgggatttacgctgatt 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 caggaatgggttgttccctgggatatggttctaacgcgggaggagcttgtaatcctgagg 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 aagtgtatgcacgtgtgcctgtgttgtgccaacattgatatcatgacgagcatgatg 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STSYGTECTYPOCA.

COMPLEMENT(31183. .31189)

COMPLEMENT(31305. .31796)

//OCHE-MORF 8; similar to human adenovirus 34 kDa

polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

7.0%; Score 62.2; DB 16; Length 34094;
Best Local Similarity 45.0%; Pred. No. 3.2e-07;
Matches 317; Conservative 0; Mismatches 383; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(33398. .33401)
complement(33768. .33771)
33951. .34094
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30590. .30940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATA_signal
TATA_signal
repeat_region
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                                                                                                                                                                            /ULTAIN 1 AL 101-"MATP PROMEDY THE ISODASEX LSPGLYOF SQATETY FILLININK
FRIPPTAPTAPTHOTTERS ORLOLF FY PURED TO YTT KTEROLANG DINKLIDMASTEPD
INGTLING PSERVEY SGTRANITHAN FRANCH PROCED TO A STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Product="100k protein"
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LADPTDEVYR TEGLGBEEPACANODLKENDSVLYELKLDNPRLAVVRQCIAVTHF
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TGGGGGGTGHTDEALGAATGSRDYSGCSARGTHSRDARRGSQURDGRURRQFAQYFRG
70089.
27769.
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DVQPIFRANQEACYAFLARHSAYFRAHRHAINEQTHLHKALDMQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /traislation="meeropenengrypppymeropoggraagasudystrnnulsagpsmigov
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tdatullonssslprsggigsegfyreevptvyinpfsgppgiypdgfianyniltds
Vagyd
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FRARCIPDSLQEGHGLRFSLPTRYSDRRHRDGDRTILTSYYCGPASFKYRCLCGHPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hexon associated protein precursor"
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                                        /codon_start=1
/product="hexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPLLLDLLCELYNRS"
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27753. .28106
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5; Gaps

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AEGLKPLKNEASFBELLSMGDSLLNDLLDIODSITOCCMKVSKYLMKDGSCASLNYY
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CEGNFLAGPEBTWYNGSGSIMPKFVQMSYABLINBANYDVTNNFARAASKGPLAI
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megonpacsrhasshsiqpoaskpkkhrnvldgaavddlkslwdrlotlogsltnwpv
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FEVLANDDEIPSIGRENAYEINSKIRVTGACYIIGNCAVLRPNIDAGEMA
FEVLANDEIPSIGRENAYEINIPDCRITATVVCCISERRYLFHNCVFSCFPHMLCLD
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FYANTLYNRYRLYMGRRGVFHPRGSTLSMCVIAAPHGVVQRIYLFGYYDATCAIMQLG
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CGLCXIKALAEEPASAGAEEEDDEVIFVSAKPGGRKRSAATPCEPDGVSKRPCVPEPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIIRVDDLQLPDPLIVMQALQRDHTLEMPRGOVDFSWIEAEERRVGPTDEWYFEAVKT
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/function="virion assembly"
/note="splice site tentative, by comparison with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .8085,12575. .12583))
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/rpt_type=inverted
/evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3225. .3536
/function="virion stability"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAB38715.1"
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/codon_start-1
/codon_start-1
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/note="large T-antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:1732268"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-NOV-1996) Campbell J.B., University of Toronto, wedical Genetics and Microbiology, 150 College Street, Toronto, Ontario MSS 3E2, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31457 GCGCAGCGGGGGGAGGAAGCAGCAGTTCACGGAGGGGGAGTGGTGGTGGTCCCGGCAGAGG 31398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31814 CGCGCGGGCCAGGTGGTGATGCGCTCCTGATGCGCGAGATCATCCGGGGCTGCGAGTAC 31755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAU77082 31323 bp DNA VRL 14-DEC-1996 Canine adenovirus type 2 strain Toronto A26/61 complete genome U77082
                                                                    31872 GGGGGGGAC--GCTGTGGAACTTTCATTGCCACTGTCTGAAAAGGTCCAGTCTGGAGTGC 31815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           763 gaggaccactgccatgttgtattctgcaggacggaggcggcggcagcagtttatt 822
                                                                                                                                                                                                                                                                                                                                                           583 ggccacgtgggttctgtggtccccgccatgagctttggatacagcgccttgcactgtggg 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           523 tttatgtccagcgtgtttatgaggggtcgccacttaatctacctgcgcttgtggtatgat 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibsta, R., Shinagawa, M., Iida, Y. and Tsukiyama, T. Nucleotide sequence of El region of canine adenovirus type Virology 172 (2), 460-467 (1989) 90021176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Canine adenovirus type 2"
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                                                                                                                                                                                                 463 aatcagaggtttatatggtaccggggaggtggtgaattacaacatgccaaaagaggtaatg
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Direct Submission
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REFERENCE AUTHORS TITLE JOURNAL MEDLINE

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AWANY YELLKULZGROWGENGGSFERVIHTCALRRNDFYFHHYAAHSADWWEKISFTPI
GAPPINTERLETYYDVETYTWHGKRFGKOLVPFMLYPOLLGDDHIVNYAKTLAREGNWEI
LESPEELTPOOLGKFKKERGKOLVPFMLYPOLLGDDHIVNYAKTLAREGNWEI
LESPEELTPOOLGKFKKEKGNPRFIEYAAVGHNITGFDEILLAAQVVSTRAEIPPYFEI
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LDNDRPAREELDVLPPFCSKGGRLCWTNEPLRGIATSIDYITHHNRGWKV
LDNRKYFEDDIESKITAKERVOLNISAKEEBAKSTRAITAGNWSITKISAFDKD
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KLAMESKGKKRIKANGKLYPEDPSNPELTRINGATVELDENDDFCLHTLEKSTPLI
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ALNRTYPSOLASSVATURDAGTPLENTEREG
ALKOTTCRKCHTVGKKLAPPENSOFLYENDAGTPLENVLKSYSTODNSLAFTREG
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ALKOTTCRKCHTVGKLARPWKNOKTLHALDMHRLIPYSKRIKY
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KOGKVFLIKDISOMOKCEFCGSFFKVTHTCALRRNDFYFHHVAAHSADWWEKISFTPI
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/function="DNA replication"
/note="prp"
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/protein_id="AAB38717.1"
/db_xref="G1:1732272"
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/note="pilla"
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/function="virion assembly"
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2607. .14040

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HIDDLINNAVUENTLARGAHVNTESDMGLKEPTRAFHGFDFFTKAUMPGFYTREF
HIDLLSFCANDFTHSRLNNFLGTRKRLPYQEGFVITWEHGFDFFTKAUMPGFYTREF
DITGGVEQIYTWASLDANYDPWTFTSSHIPSSFTFWTKSWFVANYGFALLDLERYNP
DITGGVEQIYTWASLDANYDPWTFTSSHIPSSFTFWTKSWFVANYGFALLDLERYNP
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DARRRVCPYVTKSLGVVVPRALSSKTF"

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14476

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/COGOLSTATT-I
/COGOLSTATT-I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine adenovirus type 1.

Canine adenovirus type 1.

Viruses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus. 1 (bases 1 to 199).

Sira, S., Abouhaidar, M.G., Liu, Y.C. and Campbell, J.B.

Hollippe reiteration of a 40-bp nucleotide sequence in the inverted virology 159 (1), 76-83 (1987).
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Cantiforn adenovirus type 1 E1A protein, small T-antigen, large
T-antigen, protein IX, IV22 protein, DNA polymerase, pTP, 52-55K
Protein, pilla, penton base protein, pVII protein, pV protein, we pertide precursor, pVI protein, viral protein II, endoproteinses, virion component IV, U-exon, E2A-DBP, 100 kD protein, L4-22kD protein, L4-33 kD protein, pVIII, and E4 orfill genes, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 octgggotctccactgtcattgttccagtcccggttccctgcagtgtatagccggcggc 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dragulev, B.P., Sira, Abouhaidar, M.G. and Campbell, J.B. Sequence analysis of putative E3 and fiber genomic regions of two strains of canine adenovirus type 1 Virology 183 (1), 298-305 (1991)
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Campbell,J.B. and Zhao,Y.
DNA sequence and genomic organization of canine adenovirus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416 aggittiggccagctggittaggatggiggiggatggcgccatgittaatcagaggitta 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 tatggtaccgggaggtggtgaattacaacatgccaaaagaggtaatgtttatgtccagcg 535
                                                                                                                                                                                                                                                                                                                                                                                  5.6%; Score'49.8; DB 16; Length 31323;
51.1%; Pred..No. 0.0013;
Lve 0; Mismatches 112; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536 tgittaigaggggtcgccacitaaictaccigcgctigiggtaigaigg 584
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Best Local Similarity 51.1:
Matches 117; Conservative
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JOURNAL REFERENCE

AUTHORS

TITLE JOURNAL

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FEATURES COMMENT

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BNPVSKALTAQLFYLYVQHCRDEGVLKBESLLMTAPEPESRMLVDLLMLLOTIVVQERSIL
VGEKVAAINYSVITLSKHYARKIFNSVFVPIDKEAKINTFYMRTVVQILVLSDDLGMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SY SRIKYTETHLPLOOKLINTVAANGSTINTGAYERFIDERNEETLAQVOOAVLAE
RVVADLALIRPMRGIGTTNMAGDRQVPVEGLLODHYKNLSGCONHAMGLADBEMRIONA
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TVERAGLGELEEEEMSOFWADIAYHENSGDVSEILRQVAINDTEVDSMELSFRFKVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-****
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AGATPAINSTRRYTRGAVVAQRATISISAILDNGGCVGIKYHSNIASAITAKLCNTRIX
BLAGLINRYTTVHNIAPLIEBRAASTSIIYYYGRGTVRKVEFRAEIPLISFPLKEVY
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APANTERLFIVYDVETYTWHGKFGKQLVPFMLVFOLLGDEHLVNAAKNIATTQNWOTW
NSNGTALKYCOTPERRAIGYKFKTFSTLQQHFANILWSHVLCONPKLMERAALGL
BNBGDTALKCOTPERRAIGYFFKTFSTLQGHFANILWSHVLCONPKLMERAALGL
BNBGDTALKLGTPRERAIGTPREISVYVGHYTGFDBILLAAQVVSTRAEIPPVFDIS
RNFWPRAGRILLAAQVVSTRAEIPPVFDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KOPFIAAVYGPTGGGKSQLLRNLMSAQLIVPTPETVFFITPQVDMIPPQGIAAWETQI
CEGNFLAGPENTVYPQSGSIMPRFIQMSYAQLTKDENYDVTSPNNIFANAASKGPIAI
VMDECMEDLGGNRGIAKFFRAFPSKLLDRFPKGTSVIVVLHNMPRRDQGGNIANL
KIQAKVHMISPKYHPSQLNRFINIYTKGQPTAISLLKDIFNYHRLNTNFDWIVYNTE
PIDNCHHWMILSPQEGLIPWYLNIGGKLYQALERIHRTIPPRQRWTRYYHSKRK"
complement (join (4593. 8033,12508. 12516))
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/function="DNA replication"
/note="terminal protein precursor; splice site tentative,
by comparison with human Ad2"
/note="splice site tentative, by comparison with human Ad2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"splice site tentative, by comparison with human
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/protein_id-"AAB05433.1"
/db_xref-"GI:1477659"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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SGRPLAAPRVRILYEEQQLMHIVNVILDDLKTQVAAMQNSVTAIQEELKDLKQRVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"small T-antigen"
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/product-"alid-"AAB05430.1"
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PSDSVVSEDARLDLVCAPAWSRIQIWSQAARLINDLPESVFEGGGSVVEEEGGEEHLA
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GLCYLKALAEEPYDADAGEDDEVIFVSAKRGSRKRSAVTSRGSVESSKRPCLFEPEQT
                                                                                                                                                                                                 Campbell, J.B.
Direct Submission
Submitted (14-APR-1996) James B. Campbell, University of Toronto,
Microbiology, 150 College Street, Toronto, Ontario, Canada, MSS 1A8
Microbiolature of proteins has largely followed accepted terminology
of the human adenoviruses.
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join(493. .1003.1101. .1282)
/function-"transcription activation"
/note-similar to human Ad Ela 298R protein; splice site
by comparison with canine adenovirus type 2: Shibata et
al., Virology 172 (1989) 460-467."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .30288
/organism="Canine adenovirus type 1"
/strain="CLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1406. 1915.
/function="inhibition of apoptosis"
/note="ElB 19kD protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3174. .3485 /function="virion stability"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="large T-antigen"
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/function="anti-oncogene"
/note="ElB 55kD protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="protein IX"
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1. 199
/note="left ITR"
54. 93
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                                                                                                Unpublished
4 (bases 1 to 30288)
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न्दर्शस

4.07. A. T. C.

CDS

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Voaasaryphildyeekenpdgsvsfqohergtqshengghaepaysrrolgrfy"
                                                    10798. .12489
/function="structural protein"
                                                                                                          /note="IIIa protein precursor'
/codon_start=1
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12540. 13973 /function="structural protein; virion component III"

/codon\_start=1 /product="penion base protein" /protein\_id="AABO5438.1" /db\_xref="GI:1477664"

Query Match
5.5%; Score 48.4; DB 16; Length 30288;
Best Local Similarity 50.4%; Pred. No. 0.0032;
Matches 118; Conservative 0; Mismatches 116; Indels 0;

...358 tgggctctccactgtcattgttccagtcccggttccctgcagtgtatagccggcgggcag 417 Gaps ò

ö

DD -28076 regCaacracarrencacrerrencacacrrrrscaarerrercrercrescaa 28017

...478 tggtaccgggaggtggtgaattacaacatgccaaaagaggtaatgtttatgtccagcgtg 537 **8**16

DD 27896 AIGITIAGAARCAITCATIACATITAGACTGICTITITIAGCACCGIG 27843

Search completed: June 23, 2000, 09:34:53 Job time: 12475 sec

CDS

Human secreted pro HSV-2 strain SB5 C

#11<u>--</u>

O. sativa X22 gen HSV-2 strain SB5 C Sequence encoding Cellular transcrip Measles virus AIK-ceff (ORF9) encodi Green fluorescent Cephamycin biosynt

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Disclosure; Page 37-39; 69pp; French.

Disclosure; Page 37-39; 69pp; French.

This is the sequence corresponding to nucleotides 32749-35935 of the
This is the sequence corresponding to nucleotides 32749-35935 of the
Candem repeat (ITR) region of the viral genome. The Edgregion of the
tendem repeat (ITR) region of the viral genome. The Edgregion of the
Candem contains 7 open reading frames (ORFS 1-7). These ORFs are thought
cgenome contains 7 open reading frames (ORFS 1-7). These ORFs are thought
to region of defective recombinant adenoviruses, esp. those that lack,
crowled to generate of the Edgregion. The cell lines pref. have the Edgregion inserted into their genomes for complementation of the defective
region inserted into their genomes for complementation of the defective
viruses. The Ed region is inserted under control of a promoter pref.
Crown Many (Pharmacia) which is inducible by dexamethasone. Four defective
recombinant viruses are esp. mentioned in the specification: they all
recombinant viruses are esp. mentioned in the specification: they all
clack all or part of the El region and part of the Ed region; virus AVI
clack all or part of the El region and part of the Ed region; virus AVI
clack all or part of the II region and part of the Ed region virus AVI
clack allo and 6, AV2 also lacks all of the Ed region except for ORFI (its
3303-35053), AV3 also lacks all of the Ed region except for ORFI (its
Chresent as nts 33093-33565 and 34694-33355) and AV4 further lacks the
Crows of the Ed region i.e. nts 32720-35835, 33466-33535 or 33093-35355.
Cherapy e.g. for cystic fibrosis, dystrophy, neurodegenerative diseases,
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Adenovirus E4 and part ITR region corresp. to bases 32749-35935.
Human adenovirus; inverted tandem repeat; E4; E1; Open reading frame; expression; late gene; cell line; defective recombinant adenovirus; complementation; gene therapy; cystic fibrosis; dystrophy; ds; neurodegenerative disease; blood coagulation disorder; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 96-354535/35.
Cells for prodn of recombinant adeno and adeno-associated virus
contain part of the E4 region of adeno virus, used to produce new
adeno virus defective in E1 and E4 regions for use as gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SA.
C, Perricaudet M, Vigne E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 885; DB 1; L; Pred. No. 6.8e-269; 0; Mismatches 0;
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V18266
V34209
V62169
X23525
V62176
Q99456
V18271
T00591
V71079
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JAN-1996; F00088.
20-JAN-1995; FR-000747.
01-JGN-1995; FR-006532.
(RHON ) RHONE POULENC RORER S7
Dedieu J, Latta M, Orsini C,
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Best Local Similarity 100.
Matches 885; Conservative
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WPI; 96-354535/35.
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WO9622378-Al.
25-JUL-1996.
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Measles virus Edmo
Measles virus Rube
Measles virus Mora
Measles virus Zagr
Measles virus 1977
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Chimpanzee adenovi
Adenovirus 17. Rec
Chimpanzee adenovi
                                                                                                                                             June 23, 2000, 09:05:32; Search time 56.99 Seconds (without alignments) 3885.243 Million cell updates/sec
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Second generation
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Complete sequence
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Adenovirus 5 genom
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Recombinant adenov
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Glucocorticoid rec
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Human Id-1H gene.
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                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                 Title:

Title:

GS-09-214-478-1

B85.243

Tagactacct cggcgttcc....atgac:

Sequence:

Sequence:

Introduction table:

Gapop 10.0, Gapext 1.0

Gapop 10.0, Gapext 1.0

Allses seqs, 125096042 residues

311585 seqs, 125096042 residues

Minimum DB seq length: 0

Maximum DB seq length: 1000000

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V32370
V32375
T60559
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Gaps

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Length 3189; 0; Indels

/note="specification gives this CDS at nucleotides | 15.32-24.08" | /transl\_except= (pos: 1863. .1865, aa: Tyr) /transl\_except= (pos: 2091. .2093, aa: Tyr) / 4.00. .3654

1521. .2405 /\*tag= b /product= human ?

terminator sequence"

/\*tag= c /note= "growth hormone gene

Gao G, Wilson JM;

U10245.

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Fercombinant adeno-associated virus contg. second gene which recombinant adeno-associated virus contg. second gene which acconversion from single stranded to double stranded virus - enhances efficiency of ex vivo transduction into target cell rampes - in the second sequence of a minigene containing the human adenovirus type 5 (Ad5) E4 region open reading frame (ORF) 6 under control of the mouse mammary tumour virus promoter and a growth hormone terminator sequence. The minigene is used to generate a packaging cell in expressing the E4 ORF6 product which is used to rescue and package on the deficient recombinant adeno-associated virus (rAAV). The rAAV comprises at least 2 selected genes, the first gene able to convert the single stranded virus to its double stranded form upon expression. The rAAV is useful in pharmaceutical compositions for use in ex vivo and the renet dysfunctions, e.g. cystic fibrosis.
                                                                                                                          27-0CT-1995; US-549489:
(UYPE-) UNIV PENNSILVANIA.
FISHER KJ. GAO G, WILSON J
WPI: 97-043152/04.
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05-JUN-1995;
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Oy 3361 g
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100.0%; Score 885; DB 1; L

Best Local Similarity 100.0%; Pred. No. 7.2e-269;

Matches 885; Conservative 0; Mismatches 0;
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T59270 standard; cDNA; 3653 BP.
T59270;
27-AUG-1997 (first entry)
Plasmid phwrvE40RF6 minigene sequence.
Minigene; human adenovirus type 5; open reading frame; promoter; in v mouse mammary tumour virus; growth hormone; terminator; recombinant; packaging cell line; adeno-associated virus; ex vivo; gene therapy; inherited disease; cancer; genetic dysfunction; cystic fibrosis; ds.

Location/Qualifiers
1. .1506
/\*tag= a
/note= "mouse mammary tumour virus promoter"

Synthetic. promoter 2000

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12-DEC-1996.
04-JUN-1996; U10245.
05-JUN-1995; US-462014.
27-OCT-1995; US-549489.
(UYPE-) UNIV PENNSTLVANIA.
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        27-AUG-1997 (first entry)
Second generation recombinant adenoviral vector pAV.CMVALP.GRE-ORF6.
Second generation recombinant at the first second generation adenovirus type 5; open reading frame; promoter; in vivo; mouse mammary tumour virus; growth hormone; terminator; recombinant; packeging cell line; adeno-associated virus; ex vivo; gene therapy; inherited disease; cancer; genetic dysfunction; cystic fibrosis; ds.
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/note= "cytomegalovirus enhancer/promoter"
914. . 2892
/pt.ducct= human placental alkaline phosphatase
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1547. .4713
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/note= "3' AAV ITR"
4714. .8299
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/note- "5' AAV ITR"
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Figher KX, Gao G, Wilson JM;

WET; 97-043182/04.

WET; 97-043182/04.

PT Recombinant adeno-associated virus contg. second gene which recombinant adeno-associated virus stranded to double stranded to facilitates its conversion from single stranded to double stranded to transpare to the sequence of a second generation of recombinant of this is the nucleotide sequence of a second generation of recombinant cadeno-associated virus (rAAV) which contains 2 genes, the first gene of interest (beta-qabactosidase) in the target cell; and the second gene of interest (beta-qabactosidase) in the target cell; and the second gene of interest (beta-qabactosidase) in the target cell; and the storned gene of interest (beta-qabactosidase) in the target cell; and the storned virus to its double stranded form upon expression. The rAAV is stranded virus to its double stranded form upon expression. The rAAV is therefore the treatment of inherited diseases, cancer and other genetic convertions, e.g. cystic fibrosis.
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Matches 885; Conservative
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                                                                                                                                      Value 1998 (first entry)

No. Value 1998 (first entry)

E Chimeric plasmid pav.CMVALP.GRE-ORF6.

KW acquired defects; inherited defects; genetic engineering; vector; acquired defects; inherited blosphatase; yenetic engineering; vector;

KW acquired defects; inherited defects; genetic engineering; vector;

KW acquired defects; inherited defects; genetic engineering; vector;

KW acquired dependent; alkaline phosphatase; AV.orf6; ds.

Chimeric - Squiteerin.

Chimeric - Ruman cytomegalovirus.

Chimeric - Human adenovirus 5.

KI Key

Location/Qualifiers

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Actag a

Actag a

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Anote AAV 5' inverted terminal repeat"

Attag b

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Anote CMV enhancer/promoter alkaline phosphatase (ALP)"

Anote Munan placenta alkaline phosphatase (ALP)"
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"R. 04-SEP-1997; U15694.

"R. 06-SEP-1996; US-024-100.

"A (UTPE-) UNIV PENNSTLVANIA.

"A "PATI B9-19953517.

"A "WHI! 99-19953517.

"T engineering in general

"T engineering in general

"T sequence is that of plasmid pAV. CMVALP.GRE-ORF6, also called

"A "orf6, which generates a recombinant adenovated virus

"C "A" orf6, which generates a recombinant adenovatives E4 ORF 6.

"S sequence 8299 BP; 1816 A; 2130 C; 2108 G; 1963 T;
aggacaaggcgccttatgctgcgggggggtgcgaatcatcgctgaggagaccactgccatg
                                                                                caccgccctatcctgatgcacgattatgactctaccccatgtag 885
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/note= "AAV inverted terminal repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tage c //note- human placenta alkaline | 2893. .3990 /*tag- d //note- "SY40 polyA signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4315. 45212
/*tag= 9
/note= "SV40 polyA signal"
4547. 4713
                                                                                                                                                                                                                                                                                                                                                               V22144 standard; cDNA; 8299 BP. V22144;
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V22144
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                                                                cggcgcactccgtacagtagggatcgtctacctcctttgagacagaaaccgcgctacc
                                                                       RESULT 5
V32370,c
ID V32370,c
ID V32370,c
AC V42370,
DT 29-SEP-1998 (first entry)
DE Complete sequence of the pE4/Hygro plasmid.
KW Circular, adenovirus type 5; pE4/Hygro plasmid; structural protein,
KW Complementation, E4 regulatory protein, gene therapy, HIV; tumour;
                                                                                                                                                          ö
      Length 8299;
                    Indels
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  100.0%; Score 885; DB 1; L
100.0%; Pred. No. 1.1e-268;
Live 0; Mismatches 0;
Query Match 100.
Best Local Similarity 100.
Matches 885; Conservative
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V-0-11.

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WO9813499-A2.
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KW Huntington's disease; Tay-Sachs disease; sickle cell disease;

KW marly gene; ds.

Synthetic.

ET misc_feature complement (707. 3820)

FT misc_feature (3830. 6870

FT misc_feature (380. 7000

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Best Local Similarity 100.0%; Pred. No. 1.1e-268;
Matches 885; Conservative 0; Mismatches 0;
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WPI; 98-230709/20.
Adenoviral vectors - which lack DNA encoding for structural protein 'or fibre protein used particularly for gene therapy
Example 1; Pages 131-145; 170pp; English.
The present sequence is that of a pE4/Fibre plasmid used in the method of the invention. The plasmid contains an adenovirus type 5 (AD5) method of the invention. The plasmid contains an adenovirus type 2 (AD2) tripartite leader sequence upstream of the fiber gene. The invention provides adenoviral vectors having deletions of all or part of
                                                                                                                                                                                        ttgtattcctgcaggacggacggcggcggcagtttattcgcgcgctgctgcagcac 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete sequence of the pB4/Fiber plasmid.

Circular; adenovirus type 5; pB4/Fiber plasmid; structural protein; complementation; fiber protein; gene therapy; HTV; tumour; AD5; early gene; Huntington's disease; Tay-Sachs disease; sickie cell disease; E4 regulatory gene; ds.
                                                                                                                                                                                                                                                                                                                              /*tag= a /note= "ADS E4 regulatory gene" 4051. .4366 /*tag= b /note= "ADS leader sequence" 4372. .6124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/note= "AD5 fiber gene"
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complement (21. .3149)
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24-SEP-1995; E05251.
25-SEP-1996; US-719806.
(NOVS ) NOVARTIS AG.
(SCRI ) SCRIPPS RES INST.
MEMBEROW GR. VON SEGGERN DJ.
WPI; 98-230709/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V32375 standard; DNA; 10610
V32375;
29-SEP-1998 (first_entry)
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cally region proteins. Deletions in these proteins would allow a reduced risk of wild-type virus contamination and would also allow a reduced risk of foreign DNA in such vectors for a variety of diagnostic and therapeutic applications. The adenoviral vectors having deletions in complementation of these adenoviral genes. Therefore, the pE4/Fiber plasmid was used as a complementation plasmid which was introduced into a host cell line where parts of the fiber and E4 gene region would be stably inserted into the host cell chromosomes. The resulting E4/fiber gene deficient plasmid can be used as a gene delivery vector. The gene deficient plasmid can be used as a gene delivery vector. The conditions characterised by hyper-proliferative cells (e.g. tumours), conditions characterised by hyper-proliferative cells (e.g. tumours), sickle cell diseases (e.g. Huntington's disease, Tay-Sachs disease, or sickle cell disease), or infections (e.g. HIV infection). They can also sequence 10610 BP; 2807 A; 2821 C; 2446 G; 2536 T; ö 540 907 atgaggggtcgccacttaatctacctgcgcttgtggtatgatggccacgtgggttctgtg 600 906 Arcascacrorranarcraccroscorressarascores 847 gicocogocaigagotitiggatacagogocitigcacigigggatitigaacaatatigig 660 9t9ct9tgctgcagttactgtgctgatttaagtgagatcagggtgcgctgtgtgcccgg 720 aggacaaggcgccttatgctgcgggcggtgcgaatcatcgctgaggagaccactgccatg 780 786 GIGCIGIGCIGCAGITACIGIGCIGAITIAAGIGAGAICAGGGIGGGCIGCIGIGCCCGG gene sequences encoding adenoviral 541 601 661 721 8888888888888888888 셤 à ð 셤 ò g ð g å 쉺 a ò 셤 ò

726 AGGACAAGGCGCCTTATGCTGCGGGCGGTGCGAATCATCGCTGAGGAGCCACTGCCATG 05-00398 (first entry)
Recombinant adenovirus H5.020TKneo-int.
Recombinant adenovirus H5.020TKneo-int, Adenovirus H5.020TKneo-int, plasmid padMIVneo-int; Ad5; Mo-MLV; retrovirus; retrotransposition, transposition; transposition; cratrovirus; retrotransposition; ransposition; cratrovirus; retrotransposition; cransposition; cransposition; chimeric - Mastadenovirus serotype 5.
Chimeric - Synthetic.
W09715679-Al. 882 8873 G; 841 caccgccctatcctgatgcacgattatgactctaccccatgtag 9141 C; 160559/c ID 160559 standard; DNA; 32026 BP 7388 A; 01-MAY-1997. 24-OCT-1996; U17176. 27-OCT-1995; US-005942. (UYPE-) UNIV PENNSYLVANIA. Wilson JM; 32026 BP; to empty retrovirus Kelley WM, Wilson WPI; 97-259031/23 T60559; à 음 ð 셤

Query Match
Best Local Similarity 100.0%; Score 885; DB 1; Length 32026;
Best Local Similarity 100.0%; Pred. No. 2e-268;
Matches 885; Conservative 0; Mismatches 0; Indels 0; Gaps

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                                                                                             Location/Qualiflers
8772. 9385
/*tag= a
/note= "region deleted in plasmid pdepTP and
psy611delpTP (Claim 45)"
8773. 9586
                                                                                                                                                                                                                              01/c

V07261 standard; DNA; 34303 BP.

V07261;

28-SEP-1998 (first entry)

Adenoviral vector plasmid pBHG11.

Adenovirus 5; Ad5; vector; gene therapy;

Mastadenovirus 5.
                                                                                                                                                                                                                                                    RESULT 8
V07261/C
N07261 standar
AC V07261 standar
DT 28-SEP-1998 (
DE Adenoviral vec
KW Adenoviral sy
CS Mastadenovirus
FH Key
FT misc_feature
FT misc_feature
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NPI; 98-261485/23.

Now ademoviral recombinant plasmid(s) - comprise sequences provided for expression of large foreign DNA fragments, used for, e.g. gene for expression of large foreign DNA fragments, used for, e.g. gene therefore the sequence comprises plasmid pBHGII that consists of This nucleotide sequence comprises plasmid pBHGII that consists of an EI-deleted ademovirus (Ad) genome. It contains a deletion of an EI-deleted ademovirus (Ad) genome. It contains a deletion of an EI-deleted ademovirus (Ad) genome. It contains a deletion of AdS (see also v07258) from bp 188-1339 (J.5-3, mu.). This CC AdS (see also v07258) from bp 188-1339 (J.5-3, mu.). This are perfectly contains a large deletion within the E3 region (bp BHGII also contains a large deletion within the E3 region (bp Exception removes the pascal fall and pBHGII deleted (Act E1 and CC PROMOTION PARTICLE). And pBHGII deleted (Act E1 and CC PROMOTION PARTICLE), and pBHGII (deleted for E1, polymerase as pBHGII deleted for E1, polymerase as pHGII on protice improved adenoviral vectors and packaging contains protein functions), are specifically claimed. The preterminal protein functions, and pARBGII deleted for E1, polymerase as the protein functions, are specifically claimed. The preterminal protein functions of the adenoviral vectors and packaging coll nettype of improved vector comprises deletions within the E3D region of the adenoviral genome (see also v07261).

These E3D-deleted virus are used in conjunction with novel cell inset that constitutively express E3D gene products. The invention of the adenoviral products of large genes (e.g. up to constitution provided adenoviral become and gutted vectors gene to the muscle of mice. The E3D-deleted and gutted vectors gene to the muscle of mice. The E2D-deleted and gutted vectors expensive the provided purpoved adenoviral vectors useful for a wide vectors of the packaging permit the E3D-deleted and gutted vectors of the packaging permit the packaging permit the E3D-deleted and gutted vectors of the packa
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32446 Argactacgtccggcgtrccattrggcardacactacgaccaacacgatctcggtrgrcr 32387
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/*tag= d
/note= "region deleted in plasmid
paxBdelpoldelpfpvvaRNa+t13 and
pBHG11delpolydelpfpvaRNa+t13 (Claim 53)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 34303;
/*tag= b
/note= "region deleted in plasmid
/note= paxBdelpoldelprPVARNA+ti3 and
parGildelpolydelprPVARNA+ti3 (Claim 53)'
10705. .11134
                                                                                                                         10705. .11134
/*tag= c /*tag= c /*tag= 1.0000 deleted in plasmid pdepTP and pBHG11delpTP (Claim 51)"
11067. .12513
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100.0%; Score 885; DB 1; I
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 885; Conservative 0; Mismatches 0;
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23-OCT-1997; U19541.
23-OCT-1996; US-735609.
(UNMI) UNIV MICHIGAN.
Amalfitano A. Chamberlain JS, Hartigan-OConnor DJ,
HAUSET MA, Kumar-Singhr;
WPI; 98-261485/23.
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Sequence 34303 BP; 7
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WESB80102-A.

D9-MAR-1999.

To 70-MAR-1999.

To 70-MAR-1999.

To 70-MAR-1999.

To 70-MAR-1999.

To 70-MAR-1999.

To 70-MAR-1999.

To 8-MAR-1999.

To 8-MAR-199

OC PO

the Ela and E3 regions and comprise a single packaging signal sequence and E1 and E3 regions and comprise a single packaging signal sequence and E1 and E1 and Comprise a single packaging signal sequence. The E1 deletion contains at least one Paci Clai, xbal or BstBl cleavage site. The replication deficient viral vectors can be molecules of therapeutic importance, including isoforms of the nitric contains chloride channel (CFTR) gene, the dystrophin gene, the LD receptor gene and the erythropoiethin gene. The NOS isoforms can be used in vascular applications or in cancer therapy (microphage NOS), the LD receptor gene and the erythropoiethin gene. The NOS isoforms can be used in vascular applications or in cancer therapy (microphage NOS). The coronary artery bypass grafts. A NOS containing adenovirus can also be the contained or strain and to treat second contains and to treat second contains and the erythropoieth gene can be introduced into vein grafts prior to their use as coronary artery bypass grafts. A NOS containing adenovirus can also be the contained to a strain and the erythropoieth gene can be seed following coronary arteries.

Sequence 34382 BP; 7923 A; 9880 C; 9421 G; 7158 T; replication deficient adenoviruses having deletions of 8888888888888888888888

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tacgigogaggicticccigcagigiggattiacgcigaticaggaaigggiigitccc 240 32098 TACGIGCGAGTCITCCCIGCAGIGIGGGATTTACGCIGATTCAGGAATGGGTIGITCCC 32039 Gaps 1 atgactacgtccggcgttccatttggcatgacactacgaccaacacgatctcggttgtct 60 ö Length 34382; 0; Indels Score 885; DB 1; L
Pred. No. 2.1e-268;
0; Mismatches 0; 100.0%; Ouery Match 100. Best Local Similarity 100. Matches 885; Conservative 181 g ò ŏ g 셤 ò ò g d ğ

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420 getetecactgreattgttccagtcccggttccctgcagtgtatagccggcgggcaggtt 361 31918 ò g ò g

480 ttggccagctggtttaggatggtggtggatggccatgtttaatcagaggtttatatgg 31858 g à à 셤 ò

541 atgaggggtcgccacttaatctacctgcgcttgtggtatgatggccacgtgggttctgtg 601 g a à

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100.0%; Score 885; DB 1; Length 34427; 100.0%; Pred. No. 2.1e-268;

Query Match Best Local Similarity

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DD 32569 AIGACIACGTCCGCCGTTCCATITGCCAIGACACTACGACCAACACAACTCGGTTGTCT 32510'
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601 gtcccgccatgagctttggatacagcgccttgcactgtgggattttgaacaatattgtg
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Recombinant cis-acting adenovirus H5.020TKneo-int(LTR).
Adenovirus H5.020TKneo(LTR); plasmid phadMivneo-int;
retrovirus; retrovirus); transposition; transposition; transgene;
gene therapy; vector; neomycin resistance; neo gene; ss.
Chimeric - Mastadenovirus serotype 5.
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T60557/C
T60557 standard; DNA; 35000 BP
AC T60557; standard; DNA; 36000 BP
AC T60557; standard; DNA; 36000 BP
BC T6057; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standard; standa
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WARIS 97-25901/23.

PT MOST cell chromatin in the presence of transposase, providing stable by the durable transgene expression

PS MATC cell chromatin in the presence of transposase, providing stable and durable transgene expression

PS Example 2; Fig 8A-1; 74pp; English.

CC This is the DNA sequence of the cis-acting recombinant adenovirus

CC This is the DNA sequence of the cis-acting demovirus (see 150.254) and Ad5417001. A trans-acting adenovirus (see 160.554) and Ad5417001. A trans-acting adenovirus (see 160.554) and Ad5417001. A trans-acting adenovirus (see 160.554) and Ad5417001. A trans-acting integration integration of the cis-acting terminal recombinant replication defective viruses (a) naw of, or corresponding to, at least part of the virus es. Claimed novel recombinant replication defective viruses (b) comprise: (a) DNA of, or corresponding to, at least part of the cis-acting terminal repeat sequences of a transposon, and ESI expression sequence (ESI) comprising a human gene (I) linked to the cis-acting terminal repeat sequences of a transposon, and ESI express (I) and transfer it to the cellular chromatin in vivo or in crombinant replication defective virus (B) containing a trans-acting a second expression sequence (ESI) compaining (a) as above and a second expression sequence (ESI) containing a trans-acting crombinant replication defective virus (B) containing a trans-acting and a second expression sequence (ESI) containing a trans-acting containing a trans-acting and able to express transposase in mammalian cells which stably express (I) integrated into its of or delivery and stable integration of (I) into a host cell cell-defects and able integration of (I) into a host cell cell-defects and action contains which stably express (I) integrated into its combinant retroviruses (RW) (claimed). Because (I) becomes repeated administration is avoided. The transgene is inherited by the combinant retroviruses (RW) (claimed).

Co progeny cells and the viral component is gradually degrated of comparing the
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100.0%; Score 885; DB 1; Length 35000; est.local..Similarity 100.0%; Pred. No. 2.1e-268; Efches...885; Conservative 0; Mismatches 0; Indels 0;
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  - Moloney murine leukaemia virus.
- Rattus sp.
- Synthetic.
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                                                                                  U1-MAY 11997.
24-OCT 11996; U17176.
27-OCT-11995; US-005942.
(UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                       Kelley WM, Wilson JM;
WPI; 97-259031/23.
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The adenoviral recombinant plasmid(s) - comprise sequences provided and adenoviral recombinant plasmid(s) - comprise sequences provided are therapy of genetic disease(s).

The above and a sequence comprises the adenovirus 5 (Ad5) genome. The invention provides improved adenoviral vectors and packaging within the E2b region of the adenoviral genome (see also VO726). These E2b-deleted virus are used in conjunction with novel cell inters that constitutively express E2b gene products. The invention for also provides vectors deleted for all viral coding regions. These is sho to cells, as demonstrated by the transfer of the dystrophin provides improved adenoviral vectors useful for a wide variety of gene to the muscle of mice. The E2b-deleted and gutted vectors gene to the muscle of mice and sectors useful for a wide variety of sequence 35935 BP; 8367 A; 10074 C; 9760 G; 7734 T; 30-APR-1998.
23-OCT-1996; US-735609.
(UNMI ) UNIV MICHICAN.
Amalfitano A, Chamberlain JS, Hartigan-OConnor |
Hauser MA, Rumar-Singhr; Adenovirus 5 genome. Adenovirus 5; Ad5; vector; gene therapy; ds RESULT 12 V07258/c Th V07258 standard; DNA; 35935 V07258; 28-SEP-1998 (first entry) WPI; 98-261485/23. Mastadenovirus 5. WO9817783-A1. 8 δ

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         Length 35935;
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                  Indels
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T60558, standard; DNA; 36538 BP.
AC T60558,
DT 05-MAR-1998 (first entry)
DE:..'Recombinant trans-acting adenovirus H5.020CKVgag-pol.
         Query Match
100.0%; Score 885; DB 1; L
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 885; Conservative 0; Mismatches 0;
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Example 2; Fig 9A-1; 74pp; English.

Example 2; Fig 9A-1; 74pp; English.

Example 2; Fig 9A-1; 74pp; English.

His is the DNA sequence of the trans-acting recombinant adenovirus (see Fig. 0200Mygag-pol. It was obtained by co-transfecting HEK293 and AdSI/001.

A cis-acting demonstrated in linearised plasmid paddWygag-pol (see Fig. 0200Mygag-pol.)

Calso produced, and retrotransposition and integration into host calso produced, and retrotransposition and integration into host cells was demonstrated in HeLa cells infected with both viruses.

CC laimed novel recombinant replication defective viruses (a) the comprises (b) DNA of or corresponding to, at least part of the comprises (b) DNA of or infect a mammalian cell; and (b) a first comprises of expression sequences for expression, with the cassette flanked by crequisers for expression, with the cassette flanked by required for an infect a mammalian cell and can can express (l) and transfer it to the cellular chromatin in vivo or in cerombinant replication defective virus (b) containing a trans-acting crecombinant and each of expression sequence (ES) containing a trans-acting containing a because (ii) plus regulatory sequences, flanked by bNA of containing a condition with the action of the caperated of the capera transposase (ii) integrated into its of containing a trans-acting containing a trans-acting for containing a trans-acting containing a transposase gene (ii) plus regulatory sequences, flanked by bNA of containing a transposase gene (ii) plus regulatory sequences, flanked by and (a) are used conformatin, produced by infection with (A). (A) and (B) are used conformatin, produced with conventional adenoviral vectors and the need for repeated administratio
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                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 97-259031/23.
Recombinant replication defective virus - inserts transgene into
host cell chromatin in the presence of transposase, providing stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 cggcgcactccgtacagtagggatcgtctacctccttttgagacagaaaccgcgctacc
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Adenovirus H5.020CMVgag-pol; plasmid pAdMLVneo-int; Ad5; Mo-MLV; retrovirus; retrotransposition; transgene; gene therapy; vector; ss.
Chimeric - Mastadenovirus serotype 5.
Chimeric - Moloney murine leukaemia virus.
Chimeric - Cytomegalovirus.
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11arity 100.0%; Pred. No. 2.2e-268;
Conservative 0; Mismatches 0;
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27-CT-1995; US-005942.
(UTRE) UNIV PENNSTLVANIA.
KELLEY WM. WILSON JM;
WPI; 97-259031/23.
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                 34201
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Glucocorticoid receptor/adenoviral ORF6 chimaeric fusion gene.
Glucocorticoid receptor/adenoviral ORF6 chimaeric fusion gene.
Human adenovirus; inverted tandem repeat; E4; E1; open reading frame;
expression; late gene; cell line; defective recombinant adenovirus;
complementation; gene therapy; cystic fibrosis; dystrophy; ds; PCR;
neurodegenerative disease; blood coagulation disorder; viral infection;
primer; amplification; polymerase chain reaction; fusion protein.
Homo sapiens/Adenovirus Ad5.
                                                                                                                                                                                                                                                                          AGGACAAGCCCCTTATGCTGCGGGGGGGGGAATCATCGCTGAGGAGACCACTGCCATG 33901
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1. .1605
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19-JAN-1995; FR-000747.

20-JAN-1995; FR-000747.

01-JUN-1995; FR-010547.

08-SEP-1995; FR-010541.

(RHON ) RHOME POULENC RO!

Dedieu J. Latta M, Ors.

Yeh P, Dedieu JF;

WPI: 96-354535/35;
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P-PSDB; W03197
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TDD 34200 T

OY 541 a

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Example 1; Page 40-41; 69pp; French.

Crample 1 Page 40-41; 69pp; French.

The invention relates to novel cell lines which can support the replication and production of defective recombinant adenoviruses which lack all or part of the El and E4 regions. The movel cell lines contain the adenoviral E4 region, esp. the open reading frame 6 and/or 7.

Crample 1 E4 region, esp. the open reading frame 6 and/or 7.

Crample 1 E4 region of a promoter, pref. from MMTV which is regulated by dexamethasone. The E4 OFF6 may also be inserted into the genome as a chimaeric fusion gene (this sequence) comprising a glucocorticold receptor hormone binding domain fused N terminally to the cytoplasm of the cell in the absence of hormone by interaction of the hormone binding domain with the hap90 protein or other factors.

Contacting the fusion protein with the hormone causes translocation of the protein to the cell's nucleus were the ORF6 product functions. The gene was generated by amplifying the sequence encoding the fragment with the adenoviral ORF6 sequence. The defective viruses generated in the new cells can be used for gene therapy e.g. for cystic fibrosis, characterions, etc.

Crample 1 Sequence 1 Sequence 1 Sequence 2 Sequence 1 Sequence 2 Sequence 2 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequenc
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virus defective in El and E4 regions for use as gene therapy
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Pred. No. 1.7e-268;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 884; Conservative (
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WUG9112049-A.

PD 09-UN-1994.

U1667.

PR 03-DEC-1992; U1667.

PR 01-OCT-1992; US-985478.

PR 01-OCT-1993; US-136682.

PR 13-OCT-1993; US-136742.

PR 14-OCT-1993; US-136742.

PR 14-OCT-1993; US-136742.

PR 13-OCT-1993; US-136742.

PR Adeno: Virus-based gene therapy vectors - esp. useful for gene

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PR Adeno: Virus-based gene therapy vectors - esp. useful for gene

PR Adeno: Virus-based gene therapy vectors - esp. useful for gene

PR Adeno: Virus-based gene therapy vectors - esp. useful for gene

CC adenovirus vector named Ad2-ORF6/PGK-CFTR. This virus lacks E and in its

CC adenovirus vector named Ad2-ORF6/PGK-CFTR. This virus lacks E and in its

CC place contains a modified transcription unit with the phosphoglycerate

CC promoter and a poly A addition site flanking the cystic

CK fibrosis transmembrane condutance regulator (GFTR) cDNA. The POK

CFTR oblact to shut off. The E4 region of the vactor has also been modified

CC subject to shut off. The E4 region of the vactor has also been modified

CC In that the whole sequence has been removed and replace by ORF6, the

CC only E4 gene essential for growth of adenovirus (Ad) in tissue culture.
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/note= "Represents residues 1-12914 of pAd2/PGK-CFTR"
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hort= "major late mRNA L4 poly-A signal (putative)"
1705- 31530
/*tag= u
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                                                                                                                                /note= "Major late mRNA L3 poly-A signal (putative)" complement (244729. .26318)
"major late mRNA L2 poly-A signal (putative)". 20992
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/note= "E3-2 mRNA poly-A signal (putative)"
35013. .35018
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33081. .33086
                                                                                                                                                                                                                                                                                                                                                                           /product= E3 19K protein
/note= "Glycosylated membrane protein"
31707. .32012
                                                                                                                                                                                                                                                                                                      /note= "Hexon-associated precursor" 30444. .30449
                             /*tag= n
/product= pVI protein
/note= "Hexon associated precursor"
21077. .23983
                                                                                                                                                                            "tag= q
/product= DBP protein
/note= "DNA binding or 72K protein"
26347. .28764
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                                                                                /*tag= 0
/product= Hexon protein
/note= "Virion component II"
24657. .24662
                                                                                                                                                                                                                              /*tag= r
/product= 100K protein
/note= "Hexon assembled"
29454. .30137
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/note= "pgk promoter"
1011. 5453
/*tag= ab
/product= CFTR
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/product= pvIII protein
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        /number 2
/number 2
/note= "33K protein"
13279. 14526
/*tag 9 /product= 52,55K protein
/4547. 16304
/*tag 1
/note= "Peripentonal hexon-associated protein"
16331. 16336
/*tag 1
/note= "Major late mRNA L1 poly A signal (putative)"
16390. 18105
/*tag 1
/product= Penton protein
                                                                                                                                                                                                                                                                                                                                                                                                                //note- "Represents residues 10676-34096 of Ad2-E4/ORF6" 35069. .35973
                                                            068003;
26-MR-1996 (first entry)
Ad2/-ORF6/PGK-CFTR nucledtide sequence.
Ad2/-ORF6/PGK-CFTR nucledtide sequence.
Necombinant adenovirus; Ad2/CFTR-1; adenovirus 2 serotype; Ela; Elb;
viral replication: gene expression; gene therapy; cystic fibrosis;
cystic fibrosis transmembrane conductance regulator; CFTR;
promoter; B3; p19; MHC; class 1; viral latency; pulmonary airway; ds.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                     core protein"
                                                                                                                                                                   note= "virion component III"
[8112. .18708
/*tag= k
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/product= pV protein
/note= "minor core protein"
20188. 20193
/*tag= n
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note- "Precursor to major
8778. .19887
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/note- "33K protein"
28791. .28992
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12915. .36335
/*tag= a
                                                                                                                                                                                                                                  polya_signal
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The DNA construct comprises a full length copy of the Ad2 genome from which the early region I genes (EI genes) have been deleted and replaced by an expression cassette encoding CFTR. The expression cassette horlines the promoter for PGR and a poly-A addition signal from the bovine growth hormone gene. The Ad2-ORF6/PGR-CFTR construct differs from that given in Q68002 (Ad2/CFTR-I), in that the latter utilises the endogenous BIa promoter, has no poly-A addition signal directly be administered to the pulmonary airways in the gene therapy of cystic fibrosis. 9786 G; 10000 C; 8597 A; 36335 BP; Sequence 8888888888888

0; Gaps Query Match
98.9%; Score 875.4; DB 1; Length 36335;
Best Local Similarity 99.3%; Pred. No. 2.3e-265;
Matches 879; Conservative 0; Mismatches 6; Indels 0;

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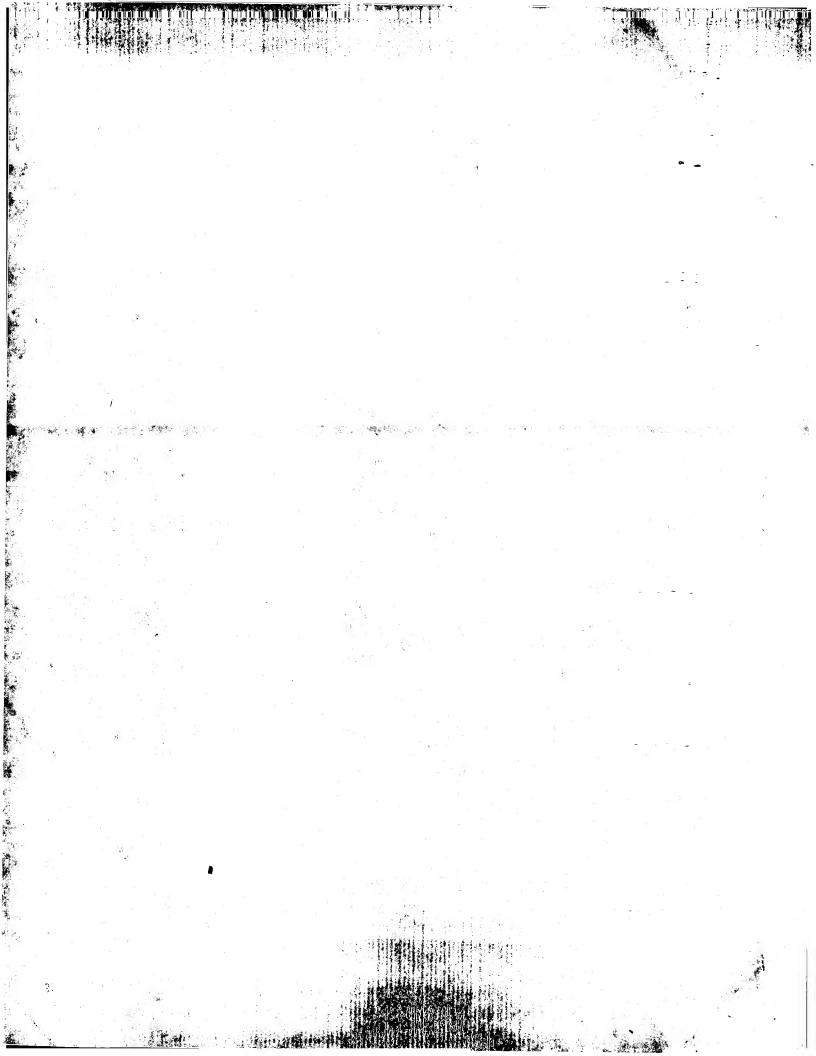
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361 35608

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Search completed: June 23, 2000, 10:05:42 Job time: 3610 sec



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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 6, Al
Sequence 1, Al
Sequence 43, Al
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Maximum DB seq length: 1000000
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Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	
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APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
APPLICANT: Fisher, Krishna J.
APPLICANT: Fisher, Krishna J.
APPLICANT: Fisher, Krishna J.
APPLICANT: Gao, Guang-Ping
TITLE OF INVENTION: Method for Improved Production of
TITLE OF INVENTION: Recombinant Adeno-Associated Viruses for Gene Therapy
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
ADDRESSEE: Howson and Howson
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                                                                                                                                                                                                    ANDKESSEE: Howson and Howson STREET: Spring House Corporate Cntr., P.O. Box 457 CITY: Spring House STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER 1947/
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,014
FILING DATE: US/08/462,014
FILING DATE: US/08/462,014
ATFORNEY/AGENT INFORMATION:
NAME: BAK, MAY E.
REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: JPHH1337USA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 118708A71ON:
TELECOMMUNICATION 118708A71ON:
TELEFRAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 3.3e-282;
Matches 885; Conservative 0; Mismatches 0;
; Sequence 2, Application US/08462014 ; Patent No. 5756283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 8299 base pairs TYPE: nucleic acid STRANDEDNESS: double
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; MOLECULE TYPE:
US-08-462-014-2
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1 atgactacgtccggcgttccatttggcatgacactacgaccaacacgatctcggttgtct 60

Suite 2200

220 Montgomery

United States Of America

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COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1..
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/735,609
FILING DATE:
CLASSIFICATION: 435
ATTORNEV/AGENT INFORMATION:
NAME: INGOLIA, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 40,027
REFERENCE/OCKET NUMBER: 40,027
REFERENCE/OCKET NUMBER: 41,05-8410
TELEFRAN: (415) 397-8338
INFORMATION FOR SEQ ID NO: TELEFRAN: (415) 397-8338
INFORMATION FOR SEQ ID NO: TELEFRAN: (415) 307-8318
INFORMATION FOR SEQ ID NO: TELEFRAN: (415) 307-8318
INFORMATION FOR SEQ ID NO: TELEFRAN: (415) 307-8318
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INFORMATION FOR SEQ ID NO: TELEFRAN: TELEFRAN: TELEFRAN:
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                         CITY: San Francisco
STATE: California
COUNTRY: United Stat
ZIP: 94104
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      3402 ATGACTACGTCCGGCGTTCCATTTGGCATGACACTACGACCAACACGATCTCGGTTGTCT 3461
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Patent No. 595360
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Rauser, Michael A.
APPLICANT: Rumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-08-735-609-4/c
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Best Local Similarity 100.0%; Pred. No. 7.1e-282;

Matches 885; Conservative 0; Mismatches 0;
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11906 AIGAGGGGTCGCCACTIAAICTACCTGCGCTTGIGGTAIGAIGGCCACGTGGGTTCTGTG 31847
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                                                                       GTCCCCGCCATGAGCTTTGGATACAGCGCCTTGCACTGTGGGGATTTTGAACAATATTGTG 31787
                                                                                                                       ttgtattcctgcaggacggagcggcggcagcagtttattcgcgcgctgctgcagcac 840
                                                                                                         gtgctgtgctgcagttactgtgctgatttaagtgagatcagggtgcgctgctgtgcccgg
                                            gtcccgccatgagctttggatacagcgccttgcactgtgggattttgaagaatattgtg
                                                                                                                                                                                                                                                                                                         11606 CACCGCCCTATCCTGATGCACGATTATGACTCTACCCCCATGTAG 31562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIOM TYPE: Floppy disk

COMPOTER: IBM PC compatible

COMPOTER: PR PC compatible

SPETATING SYSTEM: PC -DOS/MS-DOS

OPERATING SYSTEM: PATENTIN Release #1.0, Version #1.25

COURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/374,483
                                                                                                                                                                                                                                                                                         cacegecetatectgatgeacgattatgaetetaececeatgtag 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

NAME: WILSON, MARY J.

REFERENCE/DOCKET NUMBER: 1579-83

REFERENCE/DOCKET NUMBER: 1579-83
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: GEORGE, SAMUEL E.
APPLICANT: BLAZING, MICHAEL A.
TITLE OF INVENTION: ADENOVIRAL VECTOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH F
                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
105-08-374-483-6/c
56quence 6, Application US/08374483
7, Patent No. 5880102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPRONE: (703) 816-4000 TELEFAX: (703) 816-4100 TELEX: 200797 NIXN UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: DNA (genomic) US-08-374-483-6
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SEQUENCE CHARACTERISTICS
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Gaps

100.0%; Score 885; DB 3; Length 34382; 100.0%; Pred. No. 7.1e-282; .1ve 0; Mismatches 0; Indels 0;

Query Match Best Local Similarity 100.C Matches 885; Conservative ò

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31678 GICCCCGCCAIGAGCITIGGALACAGCGCCTIGCACIGIGGGAITITGAACAALATIGIG 31619
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            31979
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                                                                                                                                        32158 ATACTEGAGGATCATCCGCTGCTGCCGAATGTAACACTTTGACAATGCACAACGTGAGT 32099
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APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Hauser, Michael A.
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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Patent No. 5955360
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US-08-735-609-1/c
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APPLICANT: MEHTALI, Majid
APPLICANT: PAYIRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
TITLE OF INVENTION: COMPLEMENTATION LINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 885; DB 5; Length 35935; Pred. No. 7.2e-282;
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COUNTRY: United States
21P: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMITIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,452
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FILING DATE: 26-JAN-1995

CLASSIFICATION OF 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00624

FILING DATE: 27-MAY-1994

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00624

FILING DATE: 28-MAY-1993

ATTORNEY AGENT INFORMATION:
NAME: Dadio, Susan M.
REFERENCE/DOCKET NUMBER: 029395-002

INFORMATION FOR SEQ. ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43, Application US/08379452 Patent No. 6040174 GENERAL INFORMATION:
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US-08-379-452-43
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CORRESPONDENCE ADDRESS:
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STATE: Virginia
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Best Local Similarity
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US-08-379-452-43/c
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                                                                                                                                                                                                                       MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTREN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: INGOINA DIANE #40,027
REFERENCE/DOCKET NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0M-02484
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-838
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0%; Pred. No. 7.2e-282;
Matches 885; Conservative 0; Mismatches 0;
                                              California
: United States Of America
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 35935 base pairs
TYPE: nucleic acid
                                                                                                                              ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                  San Francisco
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CORRESPONDENCE ADDRESS:
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US-08-752-760A-1
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                                                                                                                                                                                                                                                                                    Qy <... 361.gctctccactgtcattgttccagtcccggttccctgcagtgtatagccggcgggcaggtt 420 ... 31.gctctccactgtcattgttccagttcccggttccctgcagtgtatagccggcaggtt 420 pb 33717 Gcrcccacrgrcargtrccagrcccgcrccrgcagtgtaragcccgccacgcagcargtr 33658
                                                                                                                                                                                                                                                                                                                              34017 CGGCGCACTCCGTACAGTAGGGATCGTCTACCTCCTTTTGAGACAGAAACCCGCGCTACC 33958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttgtatteetgeaggaeggaeggeggeggeagtattattegegegetgetgeageae 840
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                                                                                                          cggcgcactccgtacagtagggatcgtctacctcctttgagacagaaaccggcgctacc 120
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                                                                                                                                                                                                                                                                                                                                                                      taccgggaggtggtgaattacaacatgccaaaagaggtaatgtttatgtccagcgtgttt
                                                                                                                                                                                                                                                                                                                                                                                            33597 TACCGGGAGGTGGAATTACAACATGCCAAAAGAGGTAATGTTTATGTCCAGCGTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cacegecetateetgatgeacgattatgaetetaeeeceatgtag 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Armentano, Donna
APPLICANT: Gregory, Richard J.
APPLICANT: Smith, Alan E.
IIILE OF INVENTION: CHIMERIC ADENOVIRAL VECTORS
NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08752760A Patent No. 5877011 GENERAL INFORMATION:
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         Conservative
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US-08-752-760A-1/c
         Matches 885;
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32733 CAGCGCTTCCCCTGGTACCCCAGATTGTAACAGAAACATGCCCAAAGAGATCATGTAT 32674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32973 GAGITICCAGICCCCIGGGAIAIGAICCICACCACAGAGGAAAIAAAAAIIIIAAAAAGA 32914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33093 GAAACCAGGGCTTCACTGACTGATCAACATCCCCTGTTGCCCGATTGTGAFCATGCAGAT 33034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 33153 caarccagcresscrarcarcararcsagsscressrraccacsarcressars 33094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 gaatgggttgttccctgggatatggttctaacgcgggaggagcttgtaatcctgaggaag 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 cgatctcggttgtctcggcgcactccgtacagtagggatcgtctacctccttttgagaca 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgtatgcacgtgtgcctgtgtgccaacattgatatcatgacgagcatgatgatccat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 ggttacgagtcctgggctctccactgtcattgttccagtcccggttccatgtata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 gccggcgggcaggttttggccagctggtttaggatggtggtggatggcgccatgtttaat
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Pred. No. 5.7e-95;
0; Mismatches 308;
                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,760A
FILING DATE: 20-NOV-1996
CLASSIPICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION TELEPHONE: 212-705-5000
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Selde, Rochelle K
REGISTRATION NUMBER: 32,30
REFERENCE/DOCKET NUMBER: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.1%;
Best Local Similarity 62.4%;
Matches 520; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35081 base pairs
TYPE: nucleic acid
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
ADDRESSEE: Baker & Botts, STREET: 30 Rockefeller Pl CITY: Now York STATE: NY COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 212-705-500
TELEFAX: 212-705-5020
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); LOCATION: 22..465
; OTHER INFORMATION: /note= "CDS"
US-08-151-391A-3
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
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                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
COUNTRY: U.S.A.
2IF: 2314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN DATA:
COMPUTER: LANDV-1993
COMPUTER: LANDV-1993
COMPUTER: LANDV-1993
COMPUTER: LANDV-1993
COMPUTER: DATE: L2.NOV-1993
FILING DATE: L2.NOV-1993
CLASSIFICATION NUMBER: 34,506
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 34,506
TELEPHON: (703)684-1111
TELEPHON: (703)684-1124
TELEPHON: (703)684-1124
TELEPHON: (703)684-1124
TELEPHON: (703)684-1124
TELEPHON: CASO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: SO2 DASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                  PATENT NO. 527897

GENERAL INFORMATION:
APPLICANT: ARACA SUSUMU
APPLICANT: Makada, SUSUMU
APPLICANT: Makada, SUSUMU
APPLICANT: Makada, E1j1
APPLICANT: Makamura, Takeshi
APPLICANT: Nakamura, Takeshi
APPLICANT: Nishimoto, Toshihiko
TITLE OF INVENTION: Human ID Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
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715 gocoggagacaaggogcottatgotgogggoggtgogaatcatogotgaggagacoact 774
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Query Match
3.8%; Score 33.4; DB 1; Length 502;
Best Local Similarity 49.7%; Pred. No. 0.15;
Matches 85; Conservative 0; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                    835 cagcaccaccgccctatcctgatgcacgattatgactctacccccatgtag 885
                                                                                                                                                                                                                                                                                                                                                                                          202 GIAAACGIGCIGCICIACGACAIGAACGGCIGIIACICACGCCICAAGGAG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 12-NOV-1993
CLASSIFICATION NUMBER: 36
ATTONENTYAGENT INFORMATION:
NAME: MILLS, Demetra J.
REGISTRATION NUMBER: 34,506
REFERENCE/POCKET UNBER: 34,506
REGISTRATION NUMBER: 34,506
REGISTRATION NUMBER: 34,506
REGISTRATION NUMBER: 31,506
REGISTRATION NUMBER: 31,506
RELEFAX: (703)684-1111
TELEFAMA: (703)684-1124
TELEFAMA: (703)684-1124
TELEFAMA: (703)684-1124
TELEFAMA: (703)684-1124
TELEFAMA: (703)684-1124
TELEFAMA: (703)684-1124
TELEFAMI SO DASE DATES
SEQUENCE CHRARATERISTICS:
LENGTH: 509 base pairs
TYPE: nucleic acid
STRANDEDNES: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER STREET: 99 Canal Center Plaza, Suite 300 CITY: Alexandria COUNTY: Alexandria COUNTX: U.S.A.

ZIATE: Virginia COUNTX: U.S.A.

ZIP: 22314
COMPUTER READBALLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Oda, Kinichiro
APPLICANT: Nakada, Susumu
APPLICANT: Nakada, Susumu
APPLICANT: Yamaguchi, Tomoko
APPLICANT: Yamaguchi, Tomoko
APPLICANT: Nakamura, Takeshi
APPLICANT: Kishimoto, Toshihiko
TITLE OF INVENTION: Human ID Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-08-151-391A-1
: Sequence 1, Application US/08151391A
; Patent No. 5527897
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Length 1391;

48; Indels

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US-08-194-468-1/c

Sequence 1, Application US/08194468

Sequence 1, Application US/08194468

Sequence 1, Application US/08194468

Sequence 1, Application US/08194468

Sequence 1, Application US/08194468

Sequence 1, Application US/08194468

Parent INFORMATION: ASSAYS FOR THE IDENTIFICATION OF TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN TITLE OF INVENTION: RESPONSIVE GENES

NUMBER OF SEQUENCES: 3
                                                                                                                             259 cgggaggagcttgtaatcctgaggaagtgtatgcacgtgtgcctgtgttgtgccaacatt 318
                                                                                                                                                                                       704 cadeadercerrereaceercaegecracireacricaerrerecricescracege 645
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                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
STREET: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE STATEM FOLOS/MRS. WESTON #1.25
SOFTWARE PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,468
FILING DATE: 10-FEB-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Relier, Stephen E.
REGISTRATION NUMBER: 31,192
         3.6%; Score 32.2; DB 4;
56.0%; Pred. No. 0.63;
tive 0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)-546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (619)-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7326 base pairs
      Query Match
Best Local Similarity 56.09
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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US-08-194-468-1
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                                                                                                                                                                                                                                                                             715 geceggagaeaaggegeettatgetgegggeggtgegaateategetgaggagaeet 774
                                                                                                                                                                                                                                                                                                                                       775 gccatgitgtaticcigcaggacggagcggcggcggcagcagittaticgcgcgcigcig 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 835 cagcaccaccaccatatcctgatgcacgattatgactctacccccatgtag 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 GIABARCGIGCICTACGACAIGAACGCTGIIACICACGCCTCAAGGAG 252
                                                                                                                                                                Length 509;
                                                                                                                                                       Query Match 3.8%; Score 33.4; DB 1; Best Local Similarity 49.7%; Pred. No. 0.15; Matches 85; Conservative 0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: USA
ZIF: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBAKETTEE
COMPUTER: IBAKETTEE
COMPUTER: IBAKETTEE
COMPUTER: IBAKETTEE
COMPUTER: IBAKETTEE
COMPUTER: IBAKETTEE
COMPUTER: IBAKETEE
COMPUTER: IBAKETEE
APPLICATION NUMBER: US/08/865,336
FILING DATE: Rerewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
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REFERENCE/DOCKET NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Octoby, Neil C.
TITLE OF INVENTION: NEW HUMAN DP1 HOWOLOG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
COUNTY: Palo Alto
COUNTY: USA
ZITE: CA
; LOCATION: 22..483
; OTHER INFORMATION: /note= "CDS"
US-08-151-391A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRACTERISTICS:
LENGTH: 1391 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
ILMEDIATE SOURCE:
LIBRARY: SININOTO2
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6296 GCCATTAGCTGTGGGTTTGATTTAAGGATGTTCAGCACCTGCTGCTGCTGCTGAGGAGAG 6237

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US-08-865-336-2

Gaps

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NUCLEOTIDE SEQUENCE AND A METHOD FOR.
                                                                                                                                                                                    2516 CCTCATITIGGAACGGAGATCGCGTCTTTATIGACAGGTGGTGCTACCAACCCAATGTGCTCGAA 2575
                                                        91 cetectitigagacagaaaceegegetaceataciggaggateateegetgetgeegaa 150
84; Indels
                                                                                                                                                                                                                                                                                                                                                                                  2636 GCAAIGCCGCACIGAIACAGGAGIGGACACCCGAAICIGGIACCA 2680
                                                                                                                                                                                                                                                                                                                      211 tttacgctgattcaggaatgggttgttccctgggatatggttcta 255
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08905817

Sequence 1, Application US/08905817

Patent No. 5884710

BAPLICANT: SASAKI, Keiko

APPLICANT: MAKINO, Satoshi

TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCII

TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSE: ADDRESSE:

ADDRESSE: ADDRESSE: TOUNG & THOMPSON

STREET: 745 SOUTH 23rd Street

CITY: Arlington

STATE: USA

ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-04G-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/08/905,817
FILING DATE: 04-04G-1997
CLASSIFICATION THA:
APPLICATION NUMBER: 08/348,891
FILING DATE: 25-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/04/48,400
FILING DATE: 10-NAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05-1992
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, AND ATCH-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, AND ATCH-1991
ATTORNEY/AGENT NUMBER: 32,925
REGISTRATION NUMBER: 32,925
REGISTRATION NUMBER: 32,925
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: XP-7501A
TELEBPHONE: 703-521-2297
TELEBPHONE: 703-521-2297
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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81; Conservative
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MOLECULE TYPE: CDNA
FEATURE:
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LOCATION:
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LOCATION:
Matches
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                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: SASAKI, Keiko
APPLICANT: MORI, Takayuki
APPLICANT: MORI, Takayuki
APPLICANT: MAKINO, Satoshi
TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE,
TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US /08/348,891A
FILING DATE: 25-NOV-1994
CLISSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,400
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 3-293625
FILING DATE: 14-CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: RP-7501
TELEPHONE: 708-521-2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30.6;
Pred. No. 8;
                                                                                   Sequence 1, Application US/08348891A Patent No. 5654136
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202
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TELEFX: 248425 EMBON
INFORMATION FOR SEQ ID ##D: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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1807..3327
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5458..7107
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108..1682
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Best Local Similarity
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LOCATION:
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2304 CAGGAGGACTTCCGAGTCATGTCTCACCATCCACGACCTCCCGCCTGCGGCCACGGAA 2245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 gatatcatgacgagcatgatccatggttacgagtcctgggctctccactgtcattgt 378
                                                                                                                                                                    759 egetgaggagaceactgecatgttgtattectgeaggaeggageggeggeggeagtt 818
                                                                                                                                                                                                                                                                                   423 ceaceeceaseaccrceacaccrecrecrecaccesecesecrecescreces 482
                                                                                                                                                                                                         Query Match
Best Local Similarity 53.3%; Pred. No. 4.4;
Matches 64; Conservative 0; Mismatches 56; Indels 0;
                                                                                        Length 972;
                                                                                    3.4%; Score .v...;
53.3%; Pred. No. 2;
++ve 0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application PC/TUS9508354A
GENERAL INFORMATION:
APPLICANT: Temple University - Of The
APPLICANT: Temple University - Of The
APPLICANT: Commonwealth System of Higher Education
TITLE OF INVENTION: JAK3 PROTEIN TYROSINE
TITLE OF INVENTION: KINASE AND DNA ENCODING THE SAME
TITLE OF INVENTION: KINASE AND DNA ENCODING THE SAME
TITLE OF INVENTION: Gonda, Lavorgna
ADDRESSEE: Seldel, Gonda, Lavorgna
ADDRESSEE: & Monaco, P.C.
STREET: Sulte 1800, Two Penn Center
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19102
COMPUTER READALLE FORM:
MEDIUM TYPE: DISKette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08354A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/272,368
FILING DATE: 8 July 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4016 nucleotides
                                                                                            Query Match
Best Local Similarity 53.33
Matches 64; Conservative
          MOLECULE TYPE: CDNA PCT-US95-04801-2
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 tgtaacactttgacaatgcacaacgtgagttacgtgcgaggtcttccctgcagtgtggga 210
                                                                                                                                                                                                                                                                                                                                                                            91 cetecttttgagacagaaacecgcgctaccatactggaggatcatccgctgctgcccgaa 150
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                                                                                                                                                                                                                                                                                           Length 15894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 tttacgctgattcaggaatgggttgttccctggggatatggttcta 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04801
                                                                                                                                                                                                                                                                                           Query Match 3.5%; Score 30.6; DB 2; Best Local Similarity 49.1%; Pred. No. 8; Matches 81; Conservative 0; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Wallen III, John W.
REGISTRATION NUMBER: 3403
REFERENCE/DOCKET NUMBER: 191
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                               CDS
9234..15<u>7</u>82
                                                                                                                                       CDS
7271..9121
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5458..7107
                    CDS
3438..4442
                NAME/KEY:
LOCATION:
FEATURE:
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NAME/KEY:
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FEATURE:
LOCATION:
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US-08-905-817-1
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2244 GAICTIGGIAAAAGAACCGIGACCCAGGIICTCGIGICCCAGGCIGICCGIIGGAAIIGI 2185
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                                                                                                                                                                                                                            Sequence 1, Application US/08982956
| Patent No. 5861312
| GENERAL INFORMATION:
| APPLICANT: Warshavsky, Alexander APPLICANT: Warshavsky, Alexander APPLICANT: Warshavsky, Alexander APPLICANT: Warshavsky, Alexander APPLICANT: Word, Yong Tae TITLE OF INVENTION: NUCLEIC ACID ENCODING MANMALIAN UBRI NUMBER OF SEQUENCES: 2
| CORRESPONDENCE ADDRESS: ADDRESSE: Kevin M. Farrell, P.C. STATE: ME COUNTRY: To Box 999 CITY: York Harbor STATE: ME CONTRY: To STATE: P.C. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: WELDING WARSHING SYSTEM: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box 999 CITY: P.O. Box
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3.4%; Score 30.4; DB 3; Length 6395;
Best Local Similarity 57.3%; Pred. No. 5.7;
Matches 55; Conservative 0; Mismatches 41; Indels 0
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CLASSIFICATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: CIT-2001
TELECOMUNICATION INFORMATION:
TELEFRAX: (207) 363-0558
TELEFRAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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LOCATION: 115..5385
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MOLECULE TYPE: CDNA
FEATURE:
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US-08-982-956-1
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Search completed: June 23, 2000, 09:51:07 Job time: 6653 sec

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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9b_est41:

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                                                                                                                                                                                            June 23, 2000, 05:42:32; Search time 592.38 Seconds (without alignments) 6055.408 Million cell updates/sec
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885
1 atgactacgtccggcgttcc.....atgactctaccccatgtag 885
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                                       GenCore version 4.5
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Gapop 10.0 , Gapext 1.0
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Trotal number of hits satisfying classify and the sequents of the satisfying classify and the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the sequents of the seq
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Email: Robert Strausbergenih gov	Tissue Procurement: Andrew Barchuck M.D., John Gillespie M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can bfound through the I.M.G.E. Consortium/Link at: www-bio.llnl.gov/bbrp/image/image.html	Possible reversed clone: polyT not found Seq primer: -40Up from Gibco High quality sequence stop: 438.  Location/Qualiflers source /Organism-"Homo sapiens" /db_xref="itaxon:9606" /clone="Itaxon:9606" /clone="Itaxon:9606" /clone="itaxon:9606" /clone="itaxon:9606" /clone="itaxon:9606" /clone="itaxon:9606"	/tissue_type="endometrioid ovarian metastasis" /tlab_host="bn10p" /note="brogan: ovary; Vector: pAMP10; cDNA made by oligo-dropen: pamp10; cDNA made by oligo-dropen: pamp10. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D (NOI).  Reference: Krizman et al. (1996) Cancer Research 56:5380-5380. 56:5380-5383. 17 g 112 t 2 others	Query Match 58.9%; Score 521; DB 79; Length 564; Best Local Similarity 98.7%; Pred. No. 3.3e-147; Matches 524; Conservative 0; Mismatches 7; Indels 0; Gaps	121 atactggaggatcatccgctgctgcccgaatgtaacactttgacaatgcacaacgtgagt 180 	181	241 tgggatatggttctaacgcgggaggcttgtaatcctgaggaagtgtatgcacgtgtgc 300	301 ctgtgttgtgccaacattgatatcatgacgagcatgatgatccatggttacgagtcctgg 360 	361 gctctccactgtcattgttccagtcccggttccctgcagtgtatagccggcgggcaggtt 420 	421	481 taccgggaggtggtgaattacaacatgccaaagaggtaatgtttatgtccagcgtgttt 540 ,	541 atgaggggtcgccacttaatctacctgcgcttgtggtatgatggccacgtgggttctgtg 600 	601 gtcccgccatgagctttggatacagcgccttgcactgtgggattttgaac 651 
		नु	BAE ORJ	O m z	Qy Ub	QV Db	OY OD	OY DD	Qy Dp	Oy Dp	Oy Ob	QZ QQ	Oy Op
Score Match Length DB ID Description	521 58.9 564 79 AW265091 228.6 25.8 512 79 AW277220 228.6 25.8 515 79 AW277227 228.6 25.8 515 81 AW419027 218.8 24.7 449 80 AW340999 213.2 24.1 429 36 AA655034 201.4 22.8 30.1 36 AA659817	195.8 22.1 223 79 AW270676 43.8 4.9 630 79 AM270676 42.2 4.8 92.2 82 CNS0073W 40.4 4.5 848 82 CNS0073W 40.4 4.5 848 82 CNS0073W 39.2 4.4 1101 82 CNS00472 38.8 4.4 1101 82 CNS00472 38.4 4.3 1101 82 CNS00472 38.4 4.3 1101 83 CNS0164W 38 4.4 1101 83 CNS0164W 38 4.4 1101 83 CNS0164W 38 4.3 1101 83 CNS0164W	37 4.2 53.9 109 ACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	34.6 3.9 302 02 CNSU06QP 34.4 3.9 1101 82 CNS0038X 34.2 3.9 400 31 AA294303 34.3 3.8 600 106 AQ369543	34 3.8 791 60 AR806482 34 3.8 1101 82 CNS00BAO 33.6 3.8 339 22 R72680 33.6 3.8 415 33 AA402831	33.6 3.8 429 34 AA459525 33.6 3.8 1101 83 CNS0172T 33.4 3.8 511 23 R30064 33.4 3.8 536 63 M194566 33.4 3.8 536 63 M194566	33.2 3.8 436 61 AI874404	ALLGAMENTS		Sequence. SW265091.1 GI:6641907 EST.			on Jul 7, 1999 this sequence version replaced gi:5406367. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
NO.	00 H064067	2011 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	C 20 21 22 22 22 22 24 26 27 26 27 26 27 27 28 28 28 28 28 28 28 28 28 28 28 28 28	33.3	, o o o	) 14444 14664	4 5	RESULT	LOCUS LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE	ORGANI	AUTHORS	COMMENT

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Momo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalla;

Eukaryota: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Losses 1 to 515)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

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primine. Non-directionally cloned into the UDG sites of
primine. Non-directionally cloned into the UDG sites of
pAMP10. Size-selected on agarose appliance insert
size 500 bp. Primary library; non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW277227 515 bp mRNA EST † 03-JAN-2000 xq80a02.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756906 3' similar to SW:E417_ADE02 P03238 PROBABLE EARLY E4 17 KD PROTEIN. CONTAINS: E4 10 KD PROTEIN]. ;, mRNA sequence.
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ilarity 98.3%; Pred. No. 1.3e-58;
Conservative 0; Mismatches 4; Indels 0; Gaps
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                                      s ceacatricresiscretiscrecretracretisaritaasteasarcassiscers
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/clone_11b="NCI_CGAP_Lu34"
/tissue_type-"large cell carcinoma"
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AW277227.1 GI:6664257
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DEFINITION
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KEYWORDS
SOURCE
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                   433
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priming. Non-directionally cloned into the UDG sites of
pAMP10. Size-selected on agarose gel, average insert
size 500 bp. Primary library; non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
Reference: Krizman et al. (1996) Cancer Research
                                                                     AW277220 612 bp mRNA EST 03-JAN-2000 xq79bb6.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756819 3' similar to SW:E434_ADE02 P03239 EARLY E4 34 KD PROTEIN. ; mRNA
                                                                                                                                                                                                                                                                                       Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 612)

NCI-CGAP http://www.ncbl.nlm.nlh.gov/ncicgap.

NCI-CGAP http://www.ncbl.nlm.nlh.gov/ncicgap.

NATIONAI Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 TATTICNIGITGITGGAATGTAATACTITGATAATGTAATATGTGAGTTATGTGTGAGGT 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 catccgctgctgccgaatgtaacactttgacaatgcacaacgtgagttacgtgcgaggt 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 cttccctgcagtgtgggatttacgctgattcaggaatgggttgttccctgggatatggtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on May 18, 1998 this sequence version replaced gi.3137497.
Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
unknown ilbrary type
Possible reversed clone: polyT not found
seq primer: -40UP from Gibco
High quality sequence stop: 375.
High quality sequence stop: 375.
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56.8%; Score 503; DB 79; Length 612
Best Local Similarity 91.5%; Pred. No. 9.9e-142;
Matches 530; Conservative 0; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .612

/organism="Homo sapiens"

/organism="taxon:9606"

/clone="IMAGE:2756819"

/clone=llb=NCI_CGAP_Lu34"

/tissue_type="large cell carcinoms"

/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 g
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185 c
                                                                                                                                                                      sequence.
AW277220
AW277220.1 GI:6664250
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
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                                         RESULT 2
AW277220/c
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LOCUS DEFINITION

RESULT AW419027

δ, 8 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL COMMENT

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Institute, Cancer Genome Anatomy Project (CGAP), Institute, Cancer Genome Anatomy Project (CGAP), Institute Cancer Genome Anatomy Project (CGAP), Institute Cancer Genome Anatomy Project (CGAP), Institute Cancer Genome Anatomy Project (CGAP), Instituted (1997)

On Jan 6, 2000 this sequence version replaced gi:6677339.

Concact: Robert Strausbergenin, gov Concact: Robert Strausbergenin, gov Charles (1901), 496-1550

Email: Robert Strausbergenin, gov Charles Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

Colloe distribution: NCI-CGAP clone distribution information can be converted through the I.M.A.G.E. Consortium/LIML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: lung, Vector: pAWP10; cDNA made by oligo-dr
priming. Non-directionally cloned into the UDG sites of
PAMP10. Size-selected on agarose gel, average insert
size 500 bp. Primary library; non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
Reference: Krizman et al. (1996) Cancer Research
                                                                                                                                                                                                                                                                                                                                                              AW438779 516 bp mRNA EST 14-FEB-2000 xu38e04.xl NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2803998 ; similar to SW:E417_ADE02 P03238 PROBABLE EARLY E4 17 KD PROTEIN [CONTAINS: E4 10 KD PROTEIN].; mRNA sequence.
                                                                                               Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo. p
1 (bases 1 to 516)
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                                                                                                                                                                                             25.8%; Score 228.6; DB 81; Length 516; 98.3%; Pred. No. 1.3e-58; ive 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Possible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco High quality sequence stop: 431.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:2803998"
/clone_lib="NCI_CGAP_Lu34"
/tissue_type="large cell carcinoma"
/lab_host="PH108"
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Best Local Similarity 98.39
Matches 231; Conservative
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AW438779
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G
                                                                                                                                                                                                                                                                                                                                   AW419027 515 bp mRNA EST 09-FEB-2000 xy45f04.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2255127 3' afmilar to SW:E417_ADE02_P03238 PROBABLE EARLY E4 17 KD PROTEIN [CONTAINS: E4 10 KD PROTEIN].; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael Kelley M.D., John Gillespie M.D.,
Michael Emmert-Buck M.D., Ph.D.
GDNA Library Preparation: David B. Krizman, Ph.D.
GDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
GNA Sequencing by: Washingfor University Genome Sequencing Center
Clone distribution: NGI-GAP clone distribution information can be
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: lung, Vector: pAMP10; cDNA made by oligo-dr
priming. Non-directionally cloned into the UDG sites of
pAMP10. Size-selected on agarose gel, average insert size
500 bp. Primary library; non-amplified. cDNA Library
Preparation: David B. Krizman, Ph.D (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."
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1 (bases 1 to 515)
1 (CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
                                                                 771 cactgocatgitgiaticctgoaggacggaggggggggggggaggagtttattcgggggt 830
125 CACTGCCATGTATTCCTGCAGGACGGAGCGGCGGCGCGCAGCATTATTCGCCGCT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             711 ctgtgcccggaggacaaggcgccttatgctgcgggcggtgcgaatcatcgctgaggagac 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on wrong strand Seq primer: -400P from Glbco High quality sequence stop: 425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_"IMAGE:2856127"
/clone_lib="NCI_CGAP_Lu34.1"
/tissue_type="large_cell_carcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.515
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.8%;
Best Local Similarity 98.3%;
Matches 231; Conservative
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AW340909 AW340909.1 GI:6837535

human.

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REFERENCE AUTHORS

TITLE

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xy50e09.xl similar to sequence.

AW340909

LOCUS

RESULT AW340909

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Sequencing Center
information can be
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Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.
Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /nau_vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA652034 429 bp mRNA EST 03-NOV-1997 ns48h01.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1186897 similar to SW:E434_ADE02 P03239 EARLY E4 34 KD PROTEIN: ;, mRN
69 CCCGGAGGACAAGGCGTCTCATGCTGCGGGTGCGAATCATCGCTGACGAGACCACTG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.1%; Score 213.2; DB 36; Length 429; 96.2%; Pred. No. 5.6e-54; Brindels 1;
                                                                                                                                                       CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington University Genome St Clone distribution: NCI-CCAP clone distribution in found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:1186897"
/clone="INCI_CGAP_Alv1"
/tissue_type="alveolar rhabdomyosarcoma"
/lab_host="DH108"
                                                                                                                                    agcaccaccgccctatcctgatgcacgattatgactctacccccatgtag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seg primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-bio.llni.gov/bbrp/image/image.html
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/organism="Homo sapiens"
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Matches 229;
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AUTHORS
TITLE
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="InAGE:285661"
/clone="large cell carcinoma"
/tissue_type="large cell carcinoma"
/tab_host="DH10B"
/note="norgan: lung; vector: pAMP10; cDNA made by oligo-dT priming. Non-directionally cloned into the UDG sites of paMP10. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNB Library preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
83 a 110 c 118 g 92 t
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Tunor Gene Index.

Tunor Gene Index.

Tunor May 18, 1938 this sequence version replaced gi:3137759.

On May 18, 1938 this sequence version replaced gi:3137759.

Tuliant: Robert Strausbergenih. Gr.

Tuliant: Robert Strausbergenih. Gov.

Tuliant: Procurement: Michael Relley M.D., John Gillespie M.D.,

Tuliant: Procurement: Michael Relley M.D., John Gillespie M.D.,

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

Clone distribution: NII-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                             403 bp mRNA EST 31-JAN-2000 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856616 3' SW:E434_ADE02 P03239 EARLY E4 34 KD PROTEIN: ;, mRNA
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthoria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 403)
NCI-GGAP http://www.ncbi.nlm.nih.gov/nclogap.
NAI-GGAP http://www.ncbi.nlm.nih.gov/nclogap.
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           CIGIGCCCGGAGGACAAGGCGICTCAIGCIGCGGGCGGIGCGAAICAICGCIGAGGAGAC 137
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Matches 223; Conservative

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Similarity

Query Match

BASE COUNT ORIGIN

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AW270676 223 bp mRNA EST 03-JAN-2000 xq56b11.x1 NCI_CGAP_CO22 Homo sapiens cDNA clone IMAGE:2754621 3' similar to SW:E434_ADE02 P03239 EARLY E4 34 KD PROTEIN.;, mRNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 223)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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priming. Non-directionally cloned into the UDG sites
PAMP10. Size-selected on agarose gel, average insert
size 500 bp. Primary library; non-amplified cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
Reference: Krizman et al. (1996) Cancer Research
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Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3189136.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
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/tissue_type="colonic adenocarcinoma"
/lab_host="DH10B"
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D. Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 301)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                             301 bp mRNA EST 13-NOV-1997 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1186873 SW:E434_ADE02 P03239 EARLY E4 34 KD PROTEIN. ;, mRNA
                                    711 ctgtgccggaggacaaggcgccttatgctgcggggcggtgcgaatcatcgctgaggagac 770
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651 caatattgtggtgctgtgctgcagttactgtgctgatttaagtgagatcagggtgcgctg
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Unpublished (1997)
On Nov 29, 1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg'sth, over the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's the strausberg's 
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/organism="Homo sapiens"
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REFERENCE AUTHORS TITLE

JOURNAL COMMENT

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Tumor Gene Index
Inpublished (1997)
On Nov 22, 1999 this sequence version replaced gi:6462296.
On Nov 22, 1999 this sequence version replaced gi:6462296.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-11550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Gistribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dr
priming. Non-directionally cloned into the UDG sites of "pAMP10. Size-selected on agarose gpl, average insert
place 500 bp. Primary library; non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
                                            AW276836 630 bp mRNA EST 03-JAN-2000 xp66911.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745380 3' similar to SW:E413_ADE02 P03240 PROBABLE EARLY E4 13 KD PROTEIN. ;,
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AL066784
AL066784.1 GI:4945247
                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea; Lo 630)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="papillary serous ovarian metastasis"
/lab_host="DH10B"
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .630
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2745380"
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56:5380-5383.
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Best Local Similarity 95.7'
Matches 45; Conservative
                                                                                                                                         mRNA sequence.
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Eutheria: Primates: Catarrhini; Hominidae; Homo.

Eutheria: Primates: Catarrhini; Hominidae; Homo.

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On Sep 12, 1996 this sequence version replaced gi:1333370.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. Days Sequencing by: Washington University Genome Sequencing Conter Clone distribution: NCT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                          'AA642819 445 bp mRNA EST 27-OCT-1997 nu05b06.81 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1207091 similar to SW:E417_ADE02 P03238 PROBABLE EARLY E4 17 KD PROTEIN ; , mRNA sequence.
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Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1965) Cancer Research 56:5380-5383."
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22.0%; Score 194.6; DB 36; Length 445;
Best Local Similarity 94.9%; Pred. No. 2.5e-48;
Matches 223; Conservative 0; Mismatches 9; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 339.
Location/Qualiflers
1. .45
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMASE:1207091"
/tlssue_type="alveolar rhabdomyosarcoma"
/lab_host="lDH10B"
181 CCACCGCCCTATCCTGATGCACGATTATGACTCTACCCCCATG 223
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 848)
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927P1-4G2.TP 927P1 Trypanosoma brucei genomic clone 927P1-4G2,
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastide; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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22.6%; Pred. No. 0.18;
Live 74; Mismatches 70;
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/clone="BACR34B02",
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AQ640309.1 GI:5117019
GSS.
                      GI:4952523
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AL072642.1
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                                                     fruit fly
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                                                                                                                                     **M. Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of collaboration with the Backeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila please see http://www.fruifily.org The BDGP Drosophila and Anton Mammosar in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, EcoRI digestion of Drosophila DNA provided by the BDGP from the 150genic strain v2; on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or fillters for hybridization from the BACPAC Resource Center can be contained at http://Dacpac.med.buffalo.edu/drosophila_Dac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR34B02 of RECI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                 "Drosophija melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Etterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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4.8%; Score 42.2; DB 82;
Best Local Similarity 16.9%; Pred. No. 0.055;
Matches 60; Conservative 132; Mismatches 162;
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Trypanosoma.

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Submitted (11-70V-1999) Genoscope - Centre National de Sequencagé : ...,

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenòscope.cns.fr.

- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

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- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruutfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutovo Googewam and

melanogaster BAC library was prepared by Kazutovo Googewam and

Aaron Mammoser in Pleter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo.

Ny. The library is named RPCI-98 and was constructed by partial

Ny. The library is named RPCI-98 and was constructed by partial

ECCRI digestion of Drosophila DNA provided by the BDGP's

pland EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR48P19"
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4.4%; Score 39.2; DB 82;
Best Local Similarity 14.3%; Pred. No. 0.49;
Matches 46; Conservative 139; Mismatches 137;
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AUTHORS
TITLE
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    1 (bases 1 to 393)
E1-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujli, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Dobelson, J., Fraser, C. and Adams, M.
Determination of clone end sequences from Trypanosoma brucel TREU 927/4 Pl library
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACK48P19 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ALO78714
ALO78714. GI:5102004
                                                                                                                                                                                                                                  L Unpublished (1999)
On Mar 23, 1999 this sequence version replaced g1:3323624.
On Mar 23, 1999 this sequence version replaced g1:3323624.
On Mar 23, 1999 this sequence version replaced g1:3323624.
Other_GSSS: 927P1-462.TV
Conteact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org
For clone/filter availablilty, please contact Sara Melville
For clone/filter availablilty, Please contact Sara Melville
(sml60@mole.blo.cm.ac.uk). Pl end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: SP6
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4.5%; Score 40.2; DB 109; Length 393;
Best Local Similarity 54.4%; Pred. No. 0.15;
Matches 81; Conservative 0; Mismatches 68; Indels 0;
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1. 393
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BASE COUNT ORIGIN

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Indels

Length 1101;

406 others

641

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

RESULT 15 CNSOOLT2 LOCUS DEFINITION

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Run on:

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A52460 Sequence 4
M73260 Mastedenov1
J01917 Adenovirus
AR009152 Sequence
B62508 9E4: orf2.
AF108105 Human adenovirus
X73487 Adenovirus
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ACO08732 Homo sapi
ACO08732 Homo sapi
U68036 Streptomyce
ACO08543 Homo chr
ACO08543 Homo sapi
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AF117190 Homo sapi
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AC017390 Homo sapi
AC007734 Homo sapi
AC00774 Homo sapi
AC015350 Drosophil
AC008772 Homo sapi
AC008772 Homo sapi
AC01738 Homo sapi
AC01738 Homo sapi
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AF108105
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gb_htg14:
                                em_htg3:
em_hum5:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen. Ltd.
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Gapop 10.0 , Gapext 1.0
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Listing first 45
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Maximum DB seq length: 1000000
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NA3260 M3938
M33260.1 GI:209842
M33260.1 GI:209842

Protein 5 precursor; protein IIIa; protein V; protein pVI; protein Human adenovirus type 5
Human adenovirus type 5
VIRUSES; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

Chroboczek, J., Bieber, F. and Jacrot, B.
The sequence of the genome of adenovirus type 5 and its comparison with the genome of adenovirus type 2
VILUSES; Mastadenovirus type 2
VIRUSES; Mastadenovirus type 5 and its comparison with the genome of adenovirus type 2
VILUSES; Mastadenovirus type 2
VILUSES; Mastadenovirus type 5 and its comparison With Virology 186 (1), 280-285 (1992)
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Dedicu, J., Latta, M., Orsini, C., Perricaudet, M., Vigne, E. and Yeh, P. CELLS FOR THE PRODUCTION OF RECOMBINANT ADENOVIRUSES
Patent: WO 9622378 - A 425-JUL-1996;
RHONE POULENC RORER SA (FR)
Other publication AU 4544396 960807
Other publication FR 2729674 960726.

Location Qualifiers
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975 a 912 c 631 g 671 t
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100.0%; Score 345; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.5e-97;
Matches 345; Conservative 0; Mismatches 0;
                                                        A52460 3189 bp DNA
Sequence 4 from Patent W09622378.
A52460
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    RESULT 1
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glycoprotein: identification and structure of the signal sequence
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Osborne, T.F., Schell, R.E., Burch-Jaffe, E., Berget, S.J. and
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mitochondrial rRNA genes and three immediately adjacent
                      Natl. Acad. Sci. U.S.A. 77 (7), 3778-3782 (1980)
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The nucleotide sequence of the right-hand terminal Smal-K fragment dency trus type 2 DNA
Gene 9 (1-2), 99-114 (1980)
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canding the first leader and heterogenity at the mRNA 5' end
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Marisse,J., Courtois,G. and Galibert,F.
Nucleotide sequence of the EcoRI D fragment of adenovirus 2 Nucleic Acids Res. 8 (10), 2173-2192 (1980)
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Zain,B.S. and Roberts,R.J.
Sequences from the beginning of the fiber messenger RNA
adenovirus type 2 DNA
Biochem: Blophys. Res. Commun. 87 (3), 671-678 (1979)
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Proc. Natl. Acad. Sci. U.S.A. 77 (5), 2424-2428 (1980)
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Gene 6 (1), 1-22 (1979)
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Akusjarvi,G., Mathews,M.B., Andersson,P.,
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/translation="MKVCLIMKVEGALWELEATVEHLENRVGFDLAVCFHQHSGGERL
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1634. 1996
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Best Local Similarity 52.2
Matches 145; Conservative
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HLKVSVLVPFGYQBRALMDYHARDILTQSDVIFAGRRQELTVLLFNHTDRFLYVRK
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Human adenovirus type 9

Viruses; daDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus

1 (bases 1 to 3119)

Javier, R. and Shenk, T.
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               Unknown.
Unclassified.
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I (basss 1 to 8299)
Wilson,J.M., Fisher,K.J. and Gao,G.
Wilson,J.M., Fisher, A.J. and Gao,G.
Method for improved production of recombinant adeno-associated viruses for gene therapy patent: US 5756383-A 2 26-MAY-1998;
Patent: US 5756383-A 2 26-MAY-1998;
Location/Qualifiers
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6 genes, 3119
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23.2%; Score 80; DB 5; Length 8299;
Best Local Similarity 100.0%; Pred. No. 2.4e-14;
Matches 80; Conservative 0; Mismatches 0; Indels
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9E4: orf2. . .orf7 [adenovirus type 9, Genomic,
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Breast Cancer Res. Treat. 39 (1), 57-67 (1996)
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RESULT S82508

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ANVSLIVVSGKYQYIDHATNPTLKSFKIKLLFDNKGVLLPSSNLDSTYWNFREDNLTV
SEAYKNAVEFMPNLVAYPKPTTGSKKYARDIVYGNIYLGGLAYQPVVIKVTFNEEADS
AYSITFEFVWNKEYARVEFETTSFTFSYIAQQ"
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SANKLSLKVCHGLKTLDDKSAGGLKDLIGKLVVLTGRGIGTENLQNTDGSSRGIGISV
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MDSSQIRALVFALRPRRAEIWTWLPRGLVSLSVLEEPQGESHAGHENRIQPGPPLLKF
LLKGRAYLVDPORCEYCORFYKHQHECSYRREDFYFHINSHSNWWGEIQFF
LLKGRRYLVDPORCEYCORFYKHGHECSYRREDFYFHHINSHSNWWGEIQFF
FIGSHPRIERLEYTYDVETTWAGSFCKQLVPPMLVMKFSGPPELVALRDLARRIW
DRWERDPLIFFYCYTPREKMAVGQOFRLFRDELQYLMARELWASFMQANHLGSRALEQH
GLQCPBELTYTERLEKKLHINGRPREWELYTYOPELWEHGGCDDDSFKVQEIKVWANDT
GLQCPBELTYTERLEKKLHINGRPREWELYTYOPELWEHGGCDDDSFKVQEIKVWANDT
LNREMPRAGKILFRDYTALPUPLSKRRTDFELWEHGGCDDDSFKVQEIKVWANDT
LNREMPRAGKILFRDYTALPUPLSKRRTDFELWEHGGCDDDSFKVQEIKVWANDT
LNREMPRAGKILFRDYTALPUPLSKRRTDFELWEHGGCDDDSFKVQEIKVWANDT
GIFSEPIYYDICGMRARAALPUPROPORTHFYBELMEYRAGIRGROYPTN
IGJFSEPIYYDICGMRARAALPHWPWGPPLLKPYERMAARERWQMALDDASSKIDYFD
KKLCPGIFTIDADPEPLLLDYLPPPECSRKGGRLCWTNEPLRGEVATSVDLYTLHNG
WRWIVPDERTTYFPEWKCVARETYQLINIARGRAENDRYNDRYDGSTALLSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adenovirus type 17.

Ruman adenovirus type 17.

Ruman adenovirus type 17.

Yituses; Abna viruses, no RNA stage; Adenoviridae; Mastadenovirus.

L. (bases 1 to 35100)

Chillon, M., Bosch, A., Zabner, J., Law, L., Armentano, D., Welsh, M.J.

and Davidson, B.L.
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ALDOSDAEESEDEHRRAPFYPPSGTPGHVAYTYKPITFLDAEBGDMCHHTVEKVDPL
VDNDRY PSHVASPVLAWTRAVSEWSEELYEEDERFSTPLKGVYGDTDSLFVTER
GHRLMETRGKRAIKKRGKLAVFDEGPELTWLVEGFYCAHGGADAFAPESVFLAPKL
YALQSLLCPACGRSSKGKLRAKGHAAEALNYELMVNCYLADAGGEDRARFSYESMSLK
RTLASAQPGAHPFTVTETTLTRTLRPWKDMTLAALDAHRLVPYSRSRPNPRNEEVCHI
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Lapcapatorwplikopppphflygygylvricndyypdsrafsrlrysbydpchoty
Nwslwanctyfintgayhrfydmddfoptlyrygaliaervyadlalyoplrgygy
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AYFNY I ISNRNSNSVHRAATCLSLPCDCDWLDAFLERFSDPVDLDALTSPTPOLIRCI
VSALSLPRODPPHYREMTGGYFTLRPRERGRAVTETMRRRGEMI ERFVDRLPVRRRR
RNAPPPPPPPEEI IEVVMEEEEEDBRRGDFRREVATIAELI RLLEDELTVSARNAO
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HVELNTAQVVNARARDADGDVYYSRVWNESGLGAFSQIMGRISKNIAATVFRAGRGDLQ
EBEIEOFMSEIAYQDNSGDVQEILRQPAVNDAEIDSVELSFRFKVTGPVVFTQRRQIQ
DVNRRVVAHASALRAQHRDLPERHADVPLPFLPAGFEPPLPPGARPRHFF"
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/organism="Human adenovirus type 17"
/db_xref="taxon:46922"
complement(4991. .8266)
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Armentano, D. PhD and Souza, D.W.
Direct Submission
Submitted (20-00v-1998) Molecular Biology, Ge
New York Ave., Framinham, MA 01701-9322, USA
Location/Qualifiers
                                                                                      1871 AGGCCCATTTCTGCTGCCAGAAGTACGACAAGGTACG 1908
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Muman adenovirus type 17 complete genome.
AF108105.1 GI:4416335
241 cgcacctggttttgcttcaggaaatatgactacgtccg 278
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/db_xref="GI:4416342"
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/db_xref="G1:4416343"
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AF108105/c
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LOCUS
DEFINITION
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CDS

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complete genome; core protein; DNA polymerase; DNA-binding protein; conditions and protein; large T-antigen; maturation protein; minor core protein; penton protein; periperton protein; minor core protein; penton protein; peripentonal hexon associated protein; promoter; repeat region; mail t-antigen; transcriptional activation. Human adenovirus type 12. Human adenovirus type 12. Human adenovirus type 12. Human adenovirus type 12. Human adenovirus type 12. Human adenovirus type 12. Human adenovirus type 12. Human adenovirus type 12. Human adenovirus type 12. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 13. H
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/translation="MPLPCIPPPPVSRDTAACIAWLGLAHASCVDTLRFIKHHDLKIT
PEAEYILASLREWLYPAFLTERQRCKQKGRGAITSGRTWFCFFKYEDARKSVVYDAAR
QTVSLQIGTIQQVPTTAL"
complement(1993. .2343)
                                                                                                            /codon.start-1
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Sock.C., Iselt.A. and Doerfler.W.

A unique mitigator sequence determines the species specificity of

the major late promoter in adenovirus type 12 DNA
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Submitted (21-JUN-1993) J. Sprengel, Institute of Genetics/Dept.
Virology, Weyertal 121, 50931 Cologne 41, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1806 GCTTTTTGACGGAACGCCAACGCTGCAAAAAAAGGACGAGGTGCGATAACCAGTGGT 1747
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Pred. No. 6.8e.06;
0; Mismatches 167;
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Adenovirus type 12 DNA,
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864 c 62
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nilarity 47.8%;
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KEVMYYGSTFVRGRHLIYFKIMYDGHAWLALEKYSFGMSAFNYGILNNMLYLCCDYCK
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VERSION X51800 GI:58543

VERSION X51800.1 GI:58543

KETWORDS Human adenovirus type 12

**COGGANISM Human adenovirus type 12

**COGGANISM Human adenovirus type 12

**VIRUSES; dSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus REPERENCE 1 (Passes 1 to 3498)

AUTHORS HOGENAMP, T. and Esche, H.

**TITLE Nucleotide sequence of the right 10% of adenovirus type 12 DNA

**TITLE encoding the entire region E4

**JOURNAL Nucleic Acids Res 18 (10), 3065-3066 (1990)
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Submitted (06-FEB-1990) Hogenkamp T., Institute of Molecular
Biology (Cancer Research), University of Essex, Hufelandstr &
4300 Essen 1, F R Overlapping sequence.
Location/Qualifiers
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3
                                                                                                                                   Length 35100;
                             others
                                                                                                                                Score 54; DB 16; Length 35
Pred. No. 3.4e-06;
0; Mismatches 130; Indels
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Hogenkamp, T.
                                                                                                                                      Query Match 15.7%;
Best Local Similarity 52.2%;
Matches 145; Conservative
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YDLDVESAGEDNNAPPTILGSOPADDILEHIVDNFFNEVPSDDDLYVPSLYED
YDLDVESAGEDNNAPPTILGSOFSLILAASEGLFLPEPPYLSPVCEPIGGECMPQLHP
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1029. 1628
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WSEKSHLSWDYMLDYMSMQLWRAWLKRRVCIYSLARPLIMPPLPTLQEEKBEERNPAV
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RITVNLMSRPRLETVYWQELQDEFQRGDMHLQYKYSFEQLKTHWLEPWEDMECAIKAF
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/note="ElA; transcription activation; early protein;
alternative splicing; crossref SWISS-PROT:ELA_ADE12,
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1542. 2033
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1847. 3295
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    407
/note="crossref Ad12 EPD30061 and EPD11197"

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    34125
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/db_xref="taxon:28282"

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Shinasawa, M. and Padmanabhan, R.
Comparative sequence analysis of the inverted terminal repetitions from different adenoviruses
Froc. Natl. Acad. Sci. U.S.A. 77 (7), 3831-3835 (1980)
81054665
7 (bases 1 to 3957)
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Engler,J.A. and van Bree,M.P.
The nucleotide sequence of the gene encoding protein IVa2 in human
adenovirus type 7
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Juttermann, R., Weyer, U. and Doerfler, W.
Defect of adenovirus type 12 replication in hamster cells: absence
J. Virol. 63 (8), 3535-3540 (1989)
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Shibata, H., Zheng, J.H., Koikeda, S., Masamune, Y. and Nakanishi, Y.
Cis- and trans-acting factors for transcription of the adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     b (bases 1 to $6957)
Tolun, A., Alestrom, P. and Pettersson, U.
Sequence of inverted terminal repetitions from different
adenoviruses: demonstration of conserved sequences and homology
Cell 17 (3), 705-713 (1979)
                                                                                                                        early region 2b of
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[Cell 20 (3), 777-786 (1980)
                                                                                                                                                                                                                                                Nucleotide sequences of adenovirus DNAs
CURY. 10P. Microbiol. Immunol. 110, 73-142 (1984)
85002829
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89150250
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                                                              Variable (Passes 4831 to 10470)
Shu,L.M., Hong,J.S., Wel,Y.F. and Engler,J.A
Nucleotide sequence of the genes encoded in
human adenovirus type 12
      67 (2), 682-693 (1993)
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van Ormondt, H. and Galibert, F.
                                                                                                                                     human adenovirus type 12
Gene 46 (2-3), 187-195 (1986)
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83054637
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Kimura, T.
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DVEVDGFEEDANGEAVDGMFPERLISEAESAAESGSGDSGVGEELLPVDLDLKCYEDG
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MCALCYMRITGHCITESFISDAEGESESGSPEDTDFPHPLTATPPHGIVRTIPCRVSGR
RRPAVECIEDLLEEDPIDEPINLSLKRPKGS"
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Pienlazek, N.J., Slemenda, S.B., Pienlazek, D. and Luftig, R.B.
VA RNA region of human enteric adenovirus type 40 shows homology to the VA region of simlan adenovirus type 7
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Sussenbach, J.S.

Althogenes encoding the DNA binding protein and the 23K protease of adenovirus types 40 and 41

Virology 163, 1-10 (1988)
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Byakson, A. J., Talford, E. A., Watson, M. S., McBride, K. and Mautner, V. The DNA sequence of adenovirus type 40

J. Mol. Biol. 234 (4), 1308-1316 (1993)
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The adenovirus type 40 hexon: sequence, predicted structure and relationship to other adenovirus hexons
J. Gen. Virol. 70, 3203-3214 (1989)
                                                                Structure and organization of the left-terminal DNA regions of fastidious adenovirus types 40 and 41 Gene 58, 109-126 (1987) 88084437
                                                                                                                                                                                                                                                                      Analysis of structure and function of human adenovirus type 40 leftmost 1.85 kb region including transforming ElA gene Sapporo Igaku Zasshi 57, 59-66 (1988)
             van Loon, A. E., Ligtenberg, M., Reemst, A. M., Sussenbach, J.S. and Rozijn, T.H.
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Kidd,A.H. and Erasmus,M.J.
Sequence characterization of the adenovirus 40 fiber gene
Virology 172, 134-144 (1989)
89370295
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Ishino, M., Ohashi, Y., Emoto, T., Sawada, Y. and Fujinaga, K.
Characterization of Adenovirus type 40 El region
Virology 165, 95-102 (1988),
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join(486. 1011,1088. 1311)
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/note="for ElA"
418. .>418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hexon associated protein (Protein IX)"
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PDIITYATIGFSPLDTAAAAASAAASAATTTPAQPVTQ"
complement(3844. .5202)
/note="homologue to maturation protein Ad5, Ad2, Ad7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ademovirus type 40
Viruses; dsDNA viruses, no RNA stage; Ademoviridae; Mastademovirus.
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LVGRPKSKLSVKKCLFEKCYLALIYBGDAHIRHNAASENAGFYLLKGMALIKHNMYCG
YSODYMRFYTCADGNCHILKTVHIVSHSRHCWPVCDHNMFURCTIHLGLRRGMFRPS
QCHTSHSNIMLEPEYFSRVCLMGYFDLSVELCKVIRKNDDTRHRCRQCECGSSHIELE
PIVLNVTEELRSDHLILSCLRTDYESSDEDDN"
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Pred. No. 8.1e-06;
0; Mismatches 167; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /replace="atactgaat"
3374. .3808
/note="crossref SWISS-PROT:HEX9_ADE12,
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Human adenovirus type 40, complete genome.
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/citation=[9]
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/citation=[9]
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Best Local Similarity 47.8%;
Matches 153; Conservative 0
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                                                                   VVGRNKSQMSVKKCVFERCIMAMVVBCQARIBHNAGSDNVCFLLLKGTASVKHMMICG
GGHSQLLTCADGNCQALRVFHVVSHPRRPWPVFEHNMLMRCTVHLGARRGMFSPYQSN
                                                                                                            FCHTKVLMETDAFSRVWWNGVFDLTMELFKVVRYDESKVRCRPCECGANHIRLYPATL
                                                    VIFMNVRFVVEGFNGTVFASTTQLTLHGVFFQNCSGICVDSWGRVSARGCIFVACWKG
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Vapanstilitatigssvdtaaaaaasaaastargwaadfglxnqlaasrlreedals
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10.7%; Score 36.8; DB 16; Length;
Best Local Similarity 44.7%; Pred. No. 0.79;
Matches 143; Conservative 0; Mismatches 177; Indels
                                                                                                                               NVTEQLRIDHOMASCLRIDYESSDED"
join(1719. .1938,3061. .3149)
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3217. .3615
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3207. .>3207
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/gene="ElB"
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/gene-"E1B"
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/translation-"MRMLPDFFTGNWDDMFQGLLETEYVFDFPEPSEASEEMSLHDLF
DVEVDGFEEDANQEAVDGPISDAEGESESGSPEDTDFPHPLTATPPHGIVRTIPCRVS
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23-NOV-1999

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DNA

DEFINITION

SOURCE ORGANISM

ACCESSION VERSION KEYWORDS

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AUTHORS
TITLE
MEDLINE
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REFERENCE
TITLE
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COMMENT

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AA922842 AA514141 (Transcriptional Enhancer Factor
TEF-5) (150form 1)"
TEF-5) (150form 1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                    repeat_region
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2. (bases 1 to 170245)

Rg. Philips.S.

Rg. Philips.S.

Submitted (05-Aug-1998) E-mail enquiries: humquery@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

During sequence assembly data is comparated from overlapping clones.

Where differences are found these are annotated as variations

Where differences are found these are annotated as variations

Where differences are found these are annotated as variations

Where differences are found these are annotated as variations

Where differences are found in the sequence submitssion

corresponding to the overlapping clone, as we submit sequences

This sequence is the entire insert of clone 109F14. The true left

end of clone 329As (287822) is at 133206 in this sequence

This sequence has been finished according to sequence map criteria

as follows. An attempt is made to resolve all sequencing problems,

such as compressions and repeats, but not necessarily within known

annotated human repeat sequence elements (e.g. Alu). Where the

feature key.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Teature key.

This sequence was generated from part of bacterial clone contigs of This sequence was generated from part of bacterial sugar the Sanger human chromosome 6, constructed in collaboration by the Sanger content chromosome 6 mapping group and loannis Ragoussis. Further information can be found at http://www.sanger.ac.uk/MGP/Chrs/109F14 is from the library RDCII constructed at the Roswell Park Gancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 170245)
Tripodals, N., Mason, R., Humphray, S.J., Davies, A.F., Herberg, J.A.,
Trowsdale, J., Mason, R., Humphray, S.J., Davies, A.F., Herberg, J.A.,
Trowsdale, J., Mason, R., Engler, G. and Ragoussis, J.
Physical map of human 6p21.2-6p21.3: region flanking the
"Centromeric end of the major histocompatibility complex
Genome Res. 8 (6), 631-643 (1998)
                           Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Forcein RPLiOA gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat AL022721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL022721.1 GI:3367610
HTG; 60S Ribosomal Protein RPL10A; ca repeat polymorphism; CpG
island; NUC1; NUC1; Nuclear Hormone Receptor 1; Peroxisome
Proliferator Activated Receptor Delta; PPAR-Beta;
PPARB; PPARD; TEF-5; Transcriptional Enhancer Factor; 2NF127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="p21.2-21.3"
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/note="Alax repeat: matches 136. .5 of consensus"
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// note-MIR repeat: matches 33. .231 of consensus"

6872. .6903

// note-MIRZ repeat: matches 88. .119 of consensus"

7008. .3342

// note-"Alusg repeat: matches 1. .300 of consensus"

complement(8324. .8495)
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FEATURES

repeat; glial fibrillary acidic repetitive sequence; tandem repeat.

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join(297. .712,1563. .1623,1805. .1900,2833. .2994,3780. .3905; → 1414. .434,4408. .5451,7821. .7906,8551. .8595) dene "CGFAP"
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AHEATLARVDLERKVESLEEEIGFILRKIYEEEVRDLREQLAQQOVHVENDVARPDLTA
ALREIRTQYEAVATSNMQETEEWYRSKFADLTDAASRNAELLRQAKHEANDYRRQLQA
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HDLINVKLALDIEIATYRKLLEGEEENRITIPVQTFSNLQIRETSLDTKSVSEGHIKRN
        MMGFAPD 9971 bp DNA, ROD 10-FEB-1999 MOUSE gene for glial fibrillary acidic protein (GFAP).
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 9971)

Balcarek,J.M. and Cowan,N.J.

Structure of the mouse glial fibrillary acidic protein gene: implications for the evolution of the intermediate filament multigene family

Nucleic Acids Res. 13 (15), 5527-5543 (1985)
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/note="dinucleotide repeats (TG)6 (TC)9 (AC)8"
/gene="GFAP"
/note="Alu sequence"
/gene="GFAP"
/gene="GFAP"
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|protein_id-"CAA26571.1"
|db_xref-"GI:51066"
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    1. .9971
    /organism="Mus musculus"

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/db_xref="SWISS-PROT:P03
                                                                                                                                                                                      Alu repetitive sequence; direct protein; intermediate filament;
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/note="put. CAAT-box"
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/note="put. TATA-box"
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/gene="GFAP"
/note="intron II"
1805. .1900
/gene="GFAP"
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2377. 2432
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1563. 1623
/gene="GFAP"
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1901. .2832
/gene="GFAP"
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/gene="GFAP"
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/gene="GFAP"
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EYQVGIKAMNLDQVSKDKALQSMASMSSAQIVSASVLQNKFSPPSPLPQAVFSTSSR
WSSPPLLGGQPGPSQDIKPFAQPAYPIQPPLPSSYEPLAPLPSAAASVPVWQDRT
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KKGGLKELYERGPPNAFFLVKFWADLNSTIQEGPGAPYGVSSQYSSADSMTISVSTKV
CSFGRQVVERVVETEYARLENGRFVYRIHRSPMCEYMINFIHRLKHLPEKYMMNSVLEN
                                                                                                                                                             translation="ASNSWNASSSPGEAREDGPEGLDKGLDNDAEGVWSPDIEQSFQE"
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product-"dJ109F14.1.1 (Transcriptional Enhancer Factor
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ESTs AA134024 AA148100 AA531410 AA070054 F17880 AA641205
AA745013 AA644024 AA720704 AA888465 AA657588 AA146904
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//orde="FlAMA repeat: matches 2. .127 of consensus"
168879. 17186
//orde="AluSy repeat: matches 1. .300 of consensus"
//orde="AluSy repeat: matches 1. .300 of consensus"
//orde="MaluSy repeat: matches 128. .46 of consensus"
//orde="AluSo repeat: matches 1. .301 of consensus"
//orde="AluSo repeat: matches 2. .298 of consensus"
//orde="131339 repeat: matches 2. .298 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(12114. .12232)

complement(12114. .12232)

complement(13299. .13434)

nocte="MIR repeat: matches 211. .90 of consensus"

complement(13299. .13434)

13601. .14075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .296 of consensus'
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                                                                                  /protein_id="CAB38625.1"
/db_xref="GI:4490420"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1303. .14508
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1 Similarity 53.1%;
77; Conservative
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Matches 77; Conserv
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/note="exon 4?" 2995. .3779 /gene="GFAP"

intron

RESULT 11 MMGFAPD/c

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mRNA

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Draft entry and computer-readable sequence for [1] kindly submitted by C.Stein, 01-JUN-1989.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein; membrane-associated glycoprotein; steroid sulfatase. Human placenta, DNA to mRNA, clone 5'3.

Human placenta, DNA to mRNA, clone 5'3.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhin; Hominidae; Homo.

[ bases 1 to 2401)

[ chases 1 to 2401)

Stein,C., Hallle,A., Seidel,J., Rijnbout,S., Waheed,A., Schmidt,B., Geuze,H. and von Figura.

Cloning and expression of human steroid-sulfatase. Membrane topology, glycosylation, and subcellular distribution in BHR-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"KWHIGMSCHSKTDFCHHPLHHGFNYFYGISLTNLRDCRPGEGSV
FFTGFRRIVFLPLQIVGVTLLILAALNCLGLLHVPLGVFFSLLFLAALILTLFLGFLH
YFRPLNCFWRNYEIIQQPMSYDNLTQRLIVEAAGFIQR"
l (bases 1 to 773)
Yen,P.H., Marsh,B., Allen,E., Tsai,S.P., Ellison,J., Connolly,L.,
Yen,P.H., Marsh,B., Allen,E., Tsai,S.P., Ellison,J., Connolly,L.,
Yelsvanger, K. and Shapiro,L.J.
The human X-linked steroid sulfatase gene and a Y-encoded
pseudogene: evidence for an inversion of the Y chromosome during
primate evolution
Cell 55 (6), 1123-1135 (1988)
89077541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584 CCCTGAACTGCTTCATGATGAGGAACTACGAGATCATTCAGCAGCCCATGTCCTATGACA 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMSISB 2401 bp mRNA PRI 13-JAN-1995
Human steroid sulfatase (microsomal), complete cds.
J04964
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10.2%; Score 35.2; DB 9; Length 7;
Best Local Similarity 58.7%; Pred. No. 1.9;
Matches 61; Conservative 0; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 ctacgaccaacacgatctcggttgtctcggcgcactccgtacag 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644 ATCTCACCCAGAGGCTAACGGTGGAGGCGGCCCAGTTCATACAG 687
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89340479
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"steroid sulfatase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref-"GDB:G00-120-393"
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266. .689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      690. .>773
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/note="G00-120-393"
                                                                                                                                                                Location/Qualifiers
1. .773
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ORIGIN
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AUTHORS
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MEDLINE
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MEDLINE
FEATURES
            REFERENCE
AUTHORS
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                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMSTSXG1 773 bp DNA PRI 13-JAN-1995
Human chromosome X steroid sulfatase (STS-X) gene, exon 5 and
flanking regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="region with 19 imp. direct repeats (34 bp)"

/gene="region with 19 imp. direct repeats (34 bp)"

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/gene="region"

/note="lintron VIII"

8184. 8221

8551. >8551

8551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"intron VII"
7761. :5822
Note-": crepeats (TC)25"
5948. -6143
Noote-"region with 7 imp. direct repeats (28 bp)"
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Pred. No. 1.3;
0; Mismatches 55; Indels (
                                                                                                                                                                                                                                                     /note="intron VI"
5142. 5208
hote="homopurine sequence (GA)20 (GAA)9"
5217. 5372
/note="GT repeats (GT)24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human blood, cultured fibroblasts or tissue DNA.
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2427 c 2672 g 2392 t
                                                                                                                                     /note="intron V"
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                      /note="intron IV' 3780. .3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="exon 9"
9925. gon
                                                                                                                                                                                                                                                                                                                                                     5408. .5451
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/note="exon 7"
5452. .7820
/gene="GFAP"
                           /ou. .3905
/gene="GFAP"
/note="exon 5"
3906. 4117
                                                                                                                                                                                                 note="exon 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.6%;
Matches 69; Conservative (
                                                                                                   906. .4113
'gene="GFAP"
                                                                                                                                                                                                                      1335. .5407
'gene="GFAP"
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steroid sulfatase.
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BASE COUNT ORIGIN

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mRNA

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RESULT 12 HUMSISXG1 LOCUS DEFINITION

ORGANISM

19.11

·ACCESSION VERSION KEYWORDS SEGMENT SOURCE

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GISLTMLRDCREGEGSYFTTGFRRLYFLPLOTYGYTLTLAALNCLGLLHVPLGVFFS
LLFLAALITLIFLGFLHYFRPLNCFMNRNYEIIQQPMSYDNLTQRLYGAAGFIQRNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC005704 99033 bp DNA PRI 26-SEP-1998 AC005707 (Genome Systems Human BAC Library) complete sequence.
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1 (bases 1 to 99033)
Muzhy,D., Arenson,A.D., Adams,C., Brundage,E., Bunac,C.,
Carvelli,K., Chacko,J., Chen,J., Di,W., Ding,Y., Dugan,S.,
Durbin,J., Forcum,J., Ganesh,R., Garcia,C., Goodman,M.,
Gorrell,J.H., Haywood,M., Hernandez,J., Jackson,L., Jin,S.,
Kampal,R., Karpathy,S., Kowar,C., Leal,B., Li,Y., Lichtarge,O.,
Liu,W., Logan,O., Lu,J., Ly,T., Martinez,C., Oswal,G., Perez,L.,
Rashid,N.D., Rowland,K., Savage,L., Scherer,S.E., Shen,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 occycacctggttttgcttcaggaaatatgactacgtccggcgttccatttggcatgaca 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="steroid sulfatase precursor (EC 3.1.6.2)"
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                                                                                  a steroid sulfatase (STS) pseudogene on Yq.
Location/Qualifiers
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10.2%; Score 35.2; DB 9;
Best Local Similarity 58.7%; Pred. No. 2.2;
Matches 61; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                     /note="steroid sulfatase mRNA"
221. 286
/gene="STS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1835 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GDB:G00-120-393"
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1881 a 1440 c 1363 g 1835
Chromosome Xp22.32.
                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                       221. .1972
/gene="STS"
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                              Yen, P.H.
Unpublished (1988)
There is a steroid
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                              AUTHORS
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COMMENT
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AC005704/c
LOCUS
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FFASSGGLPDEITFAKLLKDOGTSTALIGKHIGASCHYRITHRAGELDGEGGEGE
EFTASSGGLPDEITFAKLLKDOGTSTALIGKHIGASCHYRITHRAGEGERDEGHEGEN
ELFASSGGLPDEITFAKLLKDOGTSTALIGKHIGASCHYRITHRAGEGERPELHGENYFT
ELFAALITILEGFLHYFRPLACFMENNEN EIROPMSYDNLYGGLITVABAGFTGNN
TLIFTAALITILEGFLHYFRPLACFMENNEN EIROPMSYDNLYGGLITVABAGFTGNN
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I (bases I to 2429)
Yen, P. H., Allen, E., Marsh, B., Mohandas, T., Wang, N., Taggart, R.T. and Shapiro, L.J.
Cloning and expression of steroid sulfatase cDNA and the frequent occurrence of deletions in STS deficiency: implications for X-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 cccgcacctggttttgcttcaggaaatatgactacgtccggcgttccatttggcatgaca 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    919 cccroaacriccrrcargargaacracaagarcarrcagcagcccarorccrargaca 978
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                                                                                                                                                                                               note="steroid sulfatase signal peptide A (alt.)"
                                                                                                                                                                                                                                                                 /note="steroid sulfatase precursor (EC 3.1.6.2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human placenta, cDNA to mRNA, clones M13mp18 and M13mp19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMSTS 6520 bp mRNA PRI
Human steroid sulfatase (STS) mRNA, complete cds.
M16505, 1 GI:328513
Steroid sulfatase.
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637 c 586 g 563 t
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10.2%; Score 35.2; DB 9;
Best Local Similarity 58.7%; Pred. No. 2;
Matches 61; Conservative 0; Mismatches 43;
                                                                                     note="steroid sulfatase mRNA"
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464 bp upstream of KpnI site.
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2 (bases
m.
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BASE COUNT ORIGIN

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RESULT

REFERENCE AUTHORS TITLE JOURNAL MEDLINE MEFERENCE

0; Gaps

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us-09-214-478-3.rge

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Submitted (26-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence similarities were identified using Powerblast by Jinghui Zhang.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_loss_2.2.0./
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Simon, M., Stovall, K., Timms, K.M., Todd, J., Vo, Q., Williamson, A., Worley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                  The repeat regions shown were identified using RepeatMasker by Adrian Smit.
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67. .6926
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(bases 1 to 99033)
Worley, K.C.
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/ rpt_family="LipB3"
complement(42461, .42833)
/ rpt_family="Mirial"
43873, .44173
/ rpt_family="Ralur"
/ rpt_family="MeR31B"
/ fpt_family="MeR81B"
/ folyo. .47800
/ note="Region: Similar to M16505."
                                                                               Complement (3332. 33622)

/ ppt_family="LiMB6"

Complement (3332. 33736)

/ ppt_family="LiMB6"

Complement (3374. 33797)

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/ ppt_family="THEIC"

Complement (3425. 34493)

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5053 CCCTGAACTGCTTCATGATGAGGAACTACGAGATCATTCAGCAGCCCATGTCCTATGACA 4994

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Search completed: June 23, 2000, 09:36:27 Job time: 12569 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 23, 2000, 09:07:32; Search time 20.4 Seconds (without alignments) 341.359 Million cell updates/sec

Title:

US-09-214-478-2 1594 1 MITSGVPFGMILRPIRSRLS.....RALLQHHRPILMHDYDSIPM 294

Perfect score: 1594

Sequence: 1594

I MTTSGVPFGMTLRPTRSRLS....RALLOH

Gapop 10.0, Gapext 0.5

Gapop 10.0, Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 1000000

188963

Post-processing: Minimum Match 0% Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	:	Description	100	Human Ad5 E4 regio	RAG1 pro	restri	-	`		ORF-5 protein sequ	Cytosolic glycerol	Klebsiella pneumon		Extracellular port	Mature durum wheat	Alcohol-oxidase. N	HER4 with alternat	Receptor tyrosine	HER4. New recombin	Receptor tyrosine	Human foetal brain	Rhodopsin protein.	•	nbinan	2-GM-CS	mutant	mutant	mutant	mutant	mutant	mutant		mutant	nutant	Cell cycle checkpo	Ataxia-telangiecta
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SUMMARIES		A	W03197	W01729	W41592	R37813	W48269	W01111	W92406	W03549	W57324	W60255	W30680	R08222	W62647	P60229	R54843	R91734	R54841	R91733	W82002	R38483	R93116	R11606	W19764	W19691	W19692	W19690	W19694	W19695	W19697	W19693	W19698	W19699	W19733	W3/133
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		Match Length	534	294	383	191	458	1255	1255	265	391	391	391	624	369	664	1058	1058	1308	1308	271	348	348	664	782	2998	3001	3046	3053	3054	3055	3055		3026		3020
	& Query	Match	7.66	99.3	6.4	٠	٠	4.6	4.6	4.6	4.6	4.6	4.6	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4		4.4		4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	7.	4.4
		Score	'n	1583	101.5	88.5		74	74	73.5	73	73	73	72	71	71			70.5	70.5	70	70	70	70	70	70	70	7	70	70	70	70	70	70	2	٠ 70
	Result	8	-	7	e	4	ហ	φ.	7	<b>6</b> 0	6	10	1	12	13	14	15	16	17	18	19	50	21	22	23	24	25	26	27	. 28	29	30	31	32	က်	36

Human ataxia telan ATM mutant 5319ins Muzine Ataxia-tela Polypeptide encode Canine distemper V Env polypeptide of Fragment HGJ189 o Interleukin 8 rece Recombinant high a ATM mutant C1240T.
W84269 W19696 W196178 W06813 R81304 R28033 R85644 R68811 R80756 R80951
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44444446666 44444444444
669 699 699 699 699
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## ALIGNMENTS

\* \*\*.

Gaps ö Query Match 99.7%; Score 1589; DB 1; Length 534; Best Local Similarity 100.0%; Pred. No. 2.6e-164; Matches 293; Conservative 0; Mismatches 0; Indels (

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241 RTRRIMLRAVRIIAEETTAMLYSCRTERRRQQFIRALLQHHRPILMHDYDSTPM 294 

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61 YVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRKCMHVCLCCANIDIMTSMMIYGYESW 120

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RGRHLIYLLHYDGHVGSVVPAMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCARR 241
                                                                                                    181
                                                                                                                                                                                                                  ***Human Ad5 E4 region ORF6 encoded by plasmid pAMTVE4ORF6 minigene. ****Human Ad5 E4 region ORF6 encoded by plasmid pAMTVE4ORF6 minigene. *****Minigene; human adenovirus type 5; open reading frame; promoter; in voluse mammary tumour virus; growth hormone; terminator; recombinant; packaging cell line; adeno-associated virus; ex vivo; gene therapy; inherited disease; cancer; genetic dysfunction; cystic fibrosis.
                         VRGLPCSVGFTLIQEWVVPWDMVLTREELVILRRCMHVCLCCANIDIMTSMMIHGYESWA
                                                                                               LHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFMSSVFM
                                                                                                                                                                                                                                                                                 genetic dysfunctions, e.g. cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "encoded by codon CAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encoded by codon TIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 W01729 standard; Protein; 294 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in vivo gene therapy
other genetic dysfunc
Sequence 294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
misc_difference
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Rat FRAG1 protein. Fightor activating gene 1; FRAG1; rat; FGFR2; fibroblast growth factor receptor 2; transforming activity; osteosarcoma; autophosphorylation activity; chromosomal abnormality detection;

W41592 standard; Protein; 383 AA. W41592; 18-JUN-1998 (first entry) Location/Qualifiers 1. 129 /note= "signal peptide"

Rattus sp. neoplasia.

Key Peptide

/note= "encoded by GTG" 245 /note= "encoded by CAC"

Misc\_difference

130. .383 /note= "mature FRAGI" Misc\_difference 185

18-JUN-1996; US-020009. (USSH) US DEPT HEALTH & HUMAN SERVICES. Lorenzi MV, Miki T; WPEL; 98-063151/06.

18-JUN-1997; U10660. 18-JUN-1996; US-0200

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17;
                                                                                                                                                                                                                                                  11 TLRPTRSRLSRRTPYSRDRLP------PFETETRATILEDHPLLPECNTLTM 56
                                                                                                                                                                                                                                                                     57 HNVSYVRG------LPC---SVGFTLIQEWVVPWDMVLTRE-ELVILRKCM--HV 99
                                                                                                                                                                                                                                                           40 SLRPIPERWPRLIPLLLRPAPFHSPPGWAGAPGSAPLATGVRPP--SHHYLGPSAQDPSR 97
                                                                                                                                                                                                                               Query Match 6.4%; Score 101.5; DB 1; Length 383; Best Local Similarity 22.2%; Pred. No. 0.0057; Matches 66; Conservative 36; Mismatches 106; Indels 89;
                                                                                                                                                                                                                 383 AA;
                                                                                                                                                                                                            immunoassays
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Gaps

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Score 1583; DB 1; Length 294; Pred. No. 5.1e-164; 1; Mismatches 1; Indels (

Query Match
Best Local Similarity 99.3%;
Matches 292; Conservative

61 YVRGLPCSVGFTLIQEWVVPWDAVLTREELVILRKCMHVCLCCANIDIMTSMMIHGYESW 120

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The present sequence represents RHK1 used from an example of the present invention which describes a Hansenula mrakil protease resistant killer protein. The killer protein has antibacterial activity and so can be used in an antibacterial agent which contains the killer protein as the active component. The killer protein can also be used as the active component in an antibacterial soop. The protein, which was derived from the yeast Hansenula mrakil, has antibacterial properties and may be used in sterilising and cleaning compositions e.g. soap. recombinantly in a large amount.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 MMIHGY-----ESWALHCHCSSPGSLQCIAGGQ-----VLASWFRWVVDGAMFNQRF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 VSYVRGLE-----CSVGF--TLIQEWVVPWDMVLTREELVILRKCMHVCLCCANIDIMTS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 LEVTRYPRILPDLWSSLCH---PLRKNAVLNANPAKTIPFVLIASNFIGVLFSRSLHYQF 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 VPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMM---DEEAFNDKRFHLALLISHLIALTT 317
                                                                                                                    ID NO:6 from J10075789 Example 2. HM-1; RHK1; Hansenula mrakii;
                                                                                                                                                                                                                                                                                                                                                                                    Hansenula mrakii protease resistant killer protein – has
antibacterial properties and may be used as active ingredient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
676. .1255
/label= Intracellular_domain
/note= "claimed domain, useful for immunisation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding HER-2-neu poly:peptide(s) - used for prevention or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase; breast cancer; overy cancer; colon cancer; lung cancer; prostate cancer; immunisation; tumour; vaccine; vector. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.7%; Score 75.5; DB 1; Length 458; 19.5%; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 I-WYREVVNYNMPKEVMFMSSVFMRGRHLIYLRLWYDGH 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g. soap
Example 2; Page 10-12; 16pp; Japanese.
                                                                    23-JUN-1998 (first entry)
Open reading frame RHK1 protein SEO
Killer protein; protease resistant;
yeast; mutant; antibacterial; soap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W01111 standard; Protein; 1255 AA
                                                Æ.
                                                W48269 standard; Protein; 458
                                                                                                                                                                                                                                      24-MAR-1998.
04-SEP-1996; 234393.
04-SEP-1996; JP-234393.
(EIJI-) EIJIN KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 19.5%
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-1996; U01689.
31-MAR-1995; US-414417.
(UNIW) UNIV WASHINGTON.
Cheever MA. Disis ML;
WPI, 96-455361/45.
N-PSDB; T40739.
                                                                                                                                                                                                                                                                                                                                         WPI; 98-244362/22.
N-PSDB; V20655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W01111;
01-JAN-1997 (first
HER-2/neu protein.
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W01111
RESULT
W48269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DD 24 TLHPVLELAARETPL---RLSPEDT----VVLRXHVLLEEIIERNSETFTETWNRFITHT 76

Qy 59 VS------VVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRKCMHVC--LCCA 104
98 H-CGWRRGGALEPQISFESLPCQSLACGFESDKWYQVP--LILDRDGILVRLRFIWVALI 154
                                                                                                  :| :| : |:: | :: | |: : | | :: | | :: | | :: | |:| TVCCPLVAFFFCILWSLLFHFKETTSTHCGC--PNYLPSVSSAIGGEV------ 201
                                                                                                                                                                  153 MFNQRFIWYREVVNYNMPKEVMFMSSVFMRGRHLIYLRLWYDGHVGSVVPAMSFGYSAL- 212
                                                                                                                                                                                                   201 --PQRYW-------RFCIGLHSAPRFILAFAYW-NHYLSCASPCP--GYRLLC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of EBV - for treating Espetan-Barr virus infection, infectious mononucleosis, Hodgkar's disease, Burkitt's Infection, infectious Disclosure; Page 11-12; 20pp; English: Imphoma etc.

The oligonucleotides given in 039617-18 are selectively hybridisable to the BHREI gene (039619). The antisense oligonucleotides can be used to treat EBV infection in patients suffering from infectious mononucleosis, Hodgkin's disease, Burkitt's lymphoma, undifferentiated nasopharyngeal carcinoma, AIDS related lymphoma or angioinmunoblastic lymphadenopathy. They can also be used to treat EBV-induced proliferative diseases by treating bone marrow from a patient to destroy proliferating tumour cells, then reimplanting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 EHVDLDFNSVFLEIFHRGDP-SLGRAL--AWMA-W-------CMHACRTLCCN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-----IDIMTSMMI----HGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : |: | : | : | : | : | : | 119 QSTPXYVVDLSVRGMLEASEGLDGW-IHQQ------GG-----WGTLIEDNIPGS 161
                                                                      CLCCANID----IMTSMMIHGYESWALHCHCSSPGSLQCIA---GGQVLASWFRMVVDGA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                243 RLNFSLNVVENLALLVLTYVSSSEDFTIHENA-------FIVFIAASLSYMLLTC 290
                                                                                                                                                                                                                                                                  ----HCGILNNIVVICCSYCADLSEIRVRCCARRTRRLMLRAVRIIAEETTAMLYSC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-001-1993 (first entry)
BamHI restriction fragment 1 (BHRFI) gene product.
Antisense oligonucleotide; hydridisation; EBV;
Infection; infectious mononucleosis; Hodgkin's disease;
Burkitt's lymphoma; undifferentiated nasopharyngeal carcinoma;
AIDS related lymphoma; angioimmunoblastic lymphadenopathy;
EBV-induced proliferative disease; bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New anti-sense oligo-nucleotide which hybridises with BHRFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.6%; Score 88.5; DB 1;
23.3%; Pred. No. 0.058;
tive 18; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFIWYREVVNYNMPKEVMFMSSVFMRGRH 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 RRFSWTLFLAGLTLSLLVICSYLFISRGRH 191
                                                                                                                                                                                                                                                                                                                                                                                                                                       R37813 standard; Protein; 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 23.3%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cunningham D, Hickish T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               marrow into the patient
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04-DEC-1992; G02256.
05-DEC-1991; GB-025891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epstein-Barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 93-197083/24.
N-PSDB; Q39619.
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This sequence represents the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune
                                                                                                                                                                                                                                                                                                                                                                                         387 SNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQ 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 GLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        584
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GLPCS-------KETLIQE------KVVPWDMVLTREELVILR------KCMH 98
                                                                                                                                                                                                                                                                                                                                                        ---TMHNVSY---VR 63
                             Table 2. Page 56-61; 71pp; English.

Human HER-2/neu protein (W01111), also called p185 or c-erbb2, is the product of the HER-2/neo oncogene (see also #40739). The protein is over-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, that directs expression of the polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell; B cell; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585 VACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDD---KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              507 EGLACHQL-------CARGHCWGPGPTQCVNCSQ-----F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        535 LRGQECVEECRVLQGLPRE-----YVNARHCLPCHPECQPQNGSVT---CFGPEADQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GILNNIVVLCCSYCADLSEIRVRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 VCLCCANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 IWYREVVN----YNMPKEVMFMSSVFMRGRHLIYLRLWYDGHVGSVVPAMSFGYSALHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jose of HER-2/neu polypeptides - for eliciting an immune response an HER-2/neu associated malignancy, particularly for treating or
                                                                                                                                                                                                                                                                              4.6%; Score 74; DB 1; Length 1255;
18.2%; Pred. No. 28; 'tive 34; Mismatches 117; Indels 136;
treatment of malignancies with which the HER-2/neu oncogene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676. .1255
/note= "region which elicits immune response"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 CARRTR-----RIMLRAVRIIAEETTAMLYSCRIERRRQQF----IRALLQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        642 CPAEQRASPLISIISALVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQ 692
                                                                                                                                                                                                                                                                                                                                                      20 SRRIPYSRDRLPPFETERAT ----ILEDHPLLPECNTL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human HER-2/neu oncogene protein.
HER-2/neu; oncogene; immune response;
malignancy; treatment; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W92406 standard; Protein; 1255 AA. W92406; 21-APR-1999 (first entry)
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 18.28
Matches 64, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR . 01-APR.1996; 625101.

PR . 01-APR.1996; US-625101.

PR . 12-AUG-1993; US-03364.

PR . 12-AUG-1993; US-106112.

PR . 31-MAR-1995; US-414417.

PR . (UNIW ) UNIV WASHINGTON.

PR . (Cheever MA, Disis ML;

PR . WPI: 99-152835/13.
                                                                                                                                                                                                                        1255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5869445-A.
                     associated
                                                                                                                                                                                                                            Sequence
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                64
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W92406
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ORF-5 protein sequence from BanHI fragment of HVT.
Herpes Virus of turkey; open reading frame; ORF; homology; vector;
avian herpes virus; recombinant viral vaccine; intergent region; IBDV;
cytomegalovirus immediate early promoter; UL55 gene; repeat region; ILTV;
antigen; infectious bursal disease virus; Marek's disease virus; MDV;
infectious laryngotracheitis virus; avian aneamia virus; vaccination;
infectious bronchitis virus; IBV; poultry; Gumboro disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Foldy in Taylor of the following and the follower of the follower of the follower of the follower of the follower of the follower of the follower of the follower of the follower of the protein encoded by the open that is the amino acid sequence of the protein encoded by the open that is the amino acid sequence of the protein encoded by the open reading frame 5 (ORF-5) from the Bamil I fragment from the herpes virus of turkeys (HVT). The DNA fragment was isolated from HVT strain FC126 (J. Gen. Virol., 70:1789-1804 (1989)) and is used as a basis for generating live recombinant viral vaccines using the herpes virus DNA sequences as vectors. The fragment contains 3 intergent regions into which genes encoding heterologous proteins to be expressed can be inserted, preferably under control of the cytomegalovirus immediate early (CMV-IE) promoter. The heterologous proteins can be used to vaccinate
response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence. Sequence 1255 AA;
                                                                                                                                                                                                                                                                                                    | ::| |:| ::| || ::| 387 SNTAPLQPEQLQVFETLEETIGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQ 446
                                                                                                                                                                                                                                                                                                                                                                                                   447 GLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 VCLCCANIDIMISMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRWVVDGAMFNQRF 158
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                           GLPCS-----VGFTLIQE------WVVPWDMVLTREELVILR-----KCMH 98
                                                                                                                                                                                                                                                                        ----TMHNVSY---VR 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GILNNIVVLCCSYCADLSEIRVRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | : | | : 585 VACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDD---KG
                                                                                                                                                                                                                              Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARRTR-----RIMLRAVRIIAEETTAMLYSCRTERRRQQF----IRALLQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     642 CPAEQRASPLTSIISAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQ 692
                                                                                                                                                                                  Length 1255;
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                                                                                                                                                                                4.6%; Score 74; DB 1; Le
18.2%; Pred. No. 28;
tive 34; Mismatches 117;
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30-DEC-1994; FR-016017.
(INMR) RHONE MERIEUX SA.
Audonnet JCF, Bublot MJM, E
Laplace ELF, Riviere MAE;
WPI; 96-364150/37.
                                                                                                                                                                                                       Local Similarity 18.2
nes 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Newcastle disease.
Herpesvirus of turkey
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                                                                                                                                                                                    Query Match
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Matches
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W03549
ID W0
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poultry against Gumboro disease (caused by IBDV), Newcastle disease,
Marek's disease, infectious bronchitis, infectious laryngotracheitis and
avian anaemia.
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py recontaining genes for glycerol-3-phosphate dehydrogenase and-or
py glycerol-3-phosphatese
Claim 9: Page 31-32; 57pp; English.

Claim 9: Page 31-32; 57pp; English.

Claim 9: Page 31-32; 57pp; English.

Claim 9: Page 31-32; 57pp; English.

Claim 9: Page 31-32; 57pp; English.

Claim 9: Page 31-32; 57pp; English.

Claim 9: Page 31-32; 57pp; English.

CC This Saccharomyces polypeptide comprises a cytosolic

CY 12 propertion of dlydroxyacetone phosphate to glycerol-3-phosphate.

CC Glycerol-3-phosphate (G3P) (see also cytoss 31pp) and a variety of cytoss 31pp and/or glycerol-1-phosphatese (G3P) (see also cytoss 31pp) and/or glycerol-1-phosphatese (G3P) (see also containing either a G3PpH gene and/or a G3P gene and then cultured containing either a G3PpH gene and/or a G3P gene and then cultured containing either a G3PpH gene and/or a G3P gene and then cultured containing either a G3PpH gene and/or a G3P gene and then cultured containing either a G3PpH gene and/or a G3P gene and then cultured containing eithe a monor, oligo., polysaccharde or 10-substrate.

CT be glycerol obtained is used in cosmetics, liquid soaps, the oil and fat industries. The method produces glycerol rapidly sequence 391 AA;

Sequence 391 AA;
                                                                                                                                                                                                                                                                                                                                                                              89 ELVILRK--CMHVCLCCANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                 173 QLMDSRKILCLYESAMCDN------PGAQGMILSCYCGRPGGLQCLAFIRTLEMLFN 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 HPLLPE-CNTLIMHNVSYVRGLPCSVGFTLIQEWVVPWDMVLIREELVILRKCMHVCLCC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVNYNMPKEVMFMSSVFMRGR----HLIYLRHWYDG--HVGSVVPAMSFGYSALHCGIL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                          Query Match
4.6%; Score 73.5; DB 1; Length 265;
Best Local Similarity 29.4%; Pred. No. 3.8;
Matches 20; Conservative 9; Mismatches 28; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-1998 (first entry)
Cytosolic glycerol-3-phosphate dehydrogenase GPD1.
Glycerol-3-phosphate dehydrogenase; G3PDH; GPD1; DAR1; OSG1;
D2830; YDL022W; yeast.
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4.6%; Score 73; DB 1; Length 391;
Best Local Similarity 23.2%; Pred. No. 7.4;
Matches 45; Conservative 21; Mismatches 58; Indels
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W57324;
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New method for increasing production of 1,3-propane:diol - comprises

Termentation of inexpensive carbon sources by microorganism
expressing dehydratase, used, e.g. to prolong half-life of enzyme
expressing dehydratases, used, e.g. to prolong half-life of enzyme
bisclosure; Page 65-66; 133pp; English.

The sequence is that of cytosolic glycerol-3-phosphate dehydrogenase.

The sequence is that of cytosolic glycerol-3-phosphate dehydrogenase.

I has used as part of a method of fermentative production
of 1,3-propanediol (1,3-pd), using an organism comprising
at least 1 gene encoding a dehydratase, is improved by
inserting into the host a gene encoding protein x and culturing
the transformant in presence of a carbon source (e.g. mono-, oligo-
c poly-saccharide or I substrate) convertible to 1,3-pd.

1,3-pd is a starting material for polyesters, polyurethanes and
c cyclic compounds. 1,3-pd can now be produced by a single
recombinant organism from inexpensive carbon sources such
as glucose (rather than costly glycerol or dihydroxyacetone),
c applily and without causing pollution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.6%; Score 73; DB 1; Length 391;
23.2%; Pred. No. 7.4;
Live 21; Mismatches 58; Indels
                                                                                                                                                                            Klebsiella pneumoniae glycerol-3-phosphate dehydrogenase. glycerol-3-phosphate dehydrogenase. 1,3-propanediol; recombinant. Klebsiella pneumoniae. W09821341-A2.
                                                                                                                                                                                                                                                                                   13.NOV-1997; U20873.

[13.NOV-1996; US-030601.

(GENV ) GENENCOR INT INC.

Chase MW, Dlaz-torres M, Dunn-coleman NS, Trimbur

WPI; 98-297944/26.
                                                                                                                          W60255 standard; Protein; 391 AA
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28-SEP-1998 (first entry)
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Best Local Similarity
Trans 45; Conserva'
217 NNIVVLCCSYCADL
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12-001-1998 (first entry) Glycerol-3-phosphate dehydrogenase GPD1. Glycerol-3-phosphate dehydrogenase; GPD1; 1,3-propanediol.

Saccharomyces sp. W09821339-A1. 22-MAY-1998.

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     PF 10-NOV-1997; U20292.

PA (UDUPO ) DU POWER DEMONIES & CO E I.

PA (CERW ) GENENOTE INT INC.

PI 13-NOV-1996; U302601.

PA (CERW ) GENENOTE INT INC.

PI MAGRAPHA DE NEMONIES IN THE PA (CERW ) GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GENES AND GE
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Extracellular portion of the human epidermal growth factor receptor 2.
Human epidermal growth factor receptor 2; HER2; vaccine; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 VVNYNMPKEVMFMSSVFMRGR-----HLIYLRLMYDG--HVGSVVPAMSFCYSALHCGIL 216
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13-NOV-1996; US-030601.

(DUPO) DU PONT DE NEMOURS & CO E I.

(GEMV ) GENENCOR INT INC.

Dias-Torres M, Gatenby AA, Haynie SL, Hsu AK, Lareau RD, Nagarajan V, Nair RV, Nakamura CE, Payne MS, Picataggio SK, WI: 198-297942/26.
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/label= epitope
/note= "potential T-cell epitope"
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/label= epitope
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Db 564 ------VACAHYKDPPFCVARC 579

RESULT 13
W62647

ID W62647;
DT 09-0CT-1998 (first entry)
DE Mature durum wheat glutenin protein.
KW Glutenin gene; durum wheat; low-molecular-weight; KW transgenic durum wheat.
OS Triticum durum.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 POOPPFSQQQQPVLLQQQIPFVHPSILQQLNPCKV---FLQQQCSPWAMPQSLARSQMLQ 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA sequences coding for oxido:reductase(s) and other enzyme(s) - useful for expression in microorganisms to give high yields for bleaches and detergents.

Disclosure: Fig 11A-11B: 99pp; English.

The gene encoding this protein (EC-1.1.3.13) is used (in combination with its regulatory sequences and/or those of dihydroxyacetone-synthetase) to produce genetically engineered microorganisms that produce oxidases or other enzymes in yields that allow industrial application on a large scale. The engineered yeasts can produce oxidases having improved properties with respect to their application in oxidation reactions and/or in bleaching and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 PFGMTLRPTRSR---LSRRTPYSRDRLPPFETETRATILEDHPLLP------- 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 -----ECNTLTMHNVSYVRGL-----PCSVGFTLIQEWVVPWDM--VLTREELVI 92
                                                                                                                                                                                                                                                                                             The present sequence represents the mature glutenin protein. The DNA sequence encoding this protein is isolated from the genomic DNA of Triticum durum L. The gene codes for a low-molecular-weight glutenin protein and can be used to produce transgenic durum wheat plants with "better quality characteristics" [no details given]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                Durum wheat glutenin gene – coding for glutenin protein of low
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Ledeboer AM, Verrips CT, Visser CT, Janowicz ZA, Hollenberg
WPI: 86-063249/10.
N-PSDB: N60174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Indels
                      .26-JUN-1998.

'-18-DEC-1997; 016059.

'19-DEC-1996; IT-MI2663.

(TUTY -) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.

Cardelli LE, DOVIdio R, Marchitelli C, Porceddu E;

WPI; 98-365055/32.
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11;
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Best Local Similarity 21.3%; Pred. No. 11;
Matches 29; Conservative 18; Mismatches
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                                                                                                                                                                                                                                                                   Claim 8; Page 14; 18pp; French.
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27-JUL-1984; EP-201114.
07-FEB-1985; GB-003160.
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352 LITNGIEAGVKIRPTEEELATADEDFRRGYAEYFENKPDKPLMHYSVISGFFGDHTKIPN 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The DNA encoding this sequence is identical with that of HER4 (064896) up to nucleotide 3168, where the sequence diverges and the ORF stops after 13 amino acids, followed by an extended, unique 3'-UTR where the EGFR-family of tyrosine kinases and is expressed in some human cancers and in some tissues of neuronal or muscle origin. HER4 polynucleotides, opt. labelled, are useful in assays (e.g. of HER4 mRNA to detect certain neoplasms, esp. breast carcinoma) and as primers in PCR or as probes.
                                                               89
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Human epidermal growth factor receptor; HER; EGF; tyrosihe Kinase;
cancer; neuronal tissue; muscle tissue; neoplasm;
                                                                                                               412 GKFMTMFHFLEY----PFSRGFVRITSANPYDAPDFDPGFLNDERDLWPMVWAYKKSRET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant nucleic acid expressing HER4 - a new receptor tyrosine kinase expressed in some cancer cells, and related vectors, antibodies, ligands etc, for diagnosis and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinoma; primer; probe; PCR; autophosphorylation domain;
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                                                            CNTLTM-HNVSYVRGLPCSVGFTLIQE-----
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01-JUN-1994.
23-NOV-1993; 118837.
24-NOV-1992; US-981165.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
Culouscou J, Plowman GD, Shoyab M;
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34. .3210
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R54843;
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Search completed: June 23, 2000, 10:03:34 Job time: 3362 sec

Gaps

90;

Indels

73;

DB 1; Length 664;

4.5%; Score 71; DB 19.1%; Pred. No. 25; tive 24; Mismatches

Conservative

Query Match Best Local Similarity Matches 37; Conserv

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1 MTTSGVPFGMTLRPTRSRLS......RALLQHHRPILMHDYDSTPM 294
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2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/pcTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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    protein search, using sw model

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Listing first 45 summaries
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<b>प्रयाप्यययययययययय</b>		-28 5.702897 TI SECONDATION: TI SALO, TE INVENTION: INV	larity Conservat Risrrmpys:	AARE
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		11 1 16-67-269-28  quence 28, Application tent No. 5702897  APPLICANT: Reed, John APPLICANT: Sato, Taka TITLE OF INVENTION: JANA TITLE OF INVENTION: JANA TITLE OF INVENTION: JANA TITLE OF INVENTION: JANA TOTAL A 370 La Joi CUNDERS CAUDESS ADDRESSEE: Campbell; STREET: 4370 La Joi CUNTRY: San Diego STATE: California ZIP: 90122 COMPUTER: BADABLE FORM MEDIUM TYPE: Floppy COMPUTER: TEMPORY COMPUTER: PATONION DA APPLICATION NUMBER: FILING DATE: CAMPORER: FILING DATE: JAPR APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI INFONA APPLICATION NUMBER: FILING DATE: JAPR ATTORNEY/AGNI JAPR ATTORNEY/AGN	ુ નુ ળ	:   :
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                        59 VS------YVRGLPCSVGFTLIQEWVVPWDMYLTREELVILRKCMHVC--LCCA 104
                                                                                                       -----GG-----WSTLIEDNIPGS 161
                                                                      105 N-----IDIMTSMMI---HGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.6%; Score 88.5; DB 4; Length 191; Best Local Similarity 23.3%; Pred. No. 0.013; Matches 49; Conservative 18; Mismatches 66; Indels 7
                                                                                                                                                                                                                                     RESULT 2
PCT-0595-04600-28
PCT-0595-04600-28
PCT-0595-04600-28
GENERAL INFORMATION:
APPLICANT: LA JOLIA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Interaction of Proceins Involved in TITLE OF INVENTION: a Cell Death Pathway
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRI: ...
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04600
....TNG DATE: ...12-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                      E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 TLRPTRSRLSRRTPYSRDRLPPFETETRATILEDHPLLPEC--
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119 OSTPYTVVDLSVRGMLEASEGLDGW-IHQO----
                                                                                                                                              156 QRFIWYREVVNYNWPKEVMFMSSVFMRGRH 185
                                                                                                                                                                           162 RRFSWILFLAGLTLSLLVICSYLFISRGRH 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
REFERENCE/DOCKET NUMBER: FP-LJ 1361
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (619) 525-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 191 amino acids
TYPE: amino acid
TOPOLOGY: linear
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CITY: San Diego
STATE: California
COUNTRY: USA
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. 156. QRFIWYREVVNYNMPKEVMFMSSVFMRGRH 185 162 RRFSWILFLAGLTLSLLVICSYLFISRGRH 191

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APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHIC
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 IWYREVVN----YNMPKEVMFMSSVFMRGRHLIYLRLWYDGHVGSVVPAMSFGYSALHC 213
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Best Local Similarity 18.5%; Pred. No. 0.42;
Matches 65; Conservative 34; Mismatches 116; Indels 136; Gaps
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STATE: Washington
STATE: Washington
STATE: Washington
STATE: Washington
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
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CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY,AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.446
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETAX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
TENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,083
FILLING DATE: 06-JUN-1995
CLASSIFICATION: 424
              Sequence 68, Application US/08467083 Patent No. 5726023 GENERAL INFORMATION:
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and
                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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TOPOLOGY:
US-08-467-083-68
US-08-467-083-68
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CITY: Seattle
STATE: Washing
US-08-486-348A-68
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                                                                                     GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
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Best Local Similarity 18.5%; Pred. No. 0.42;
Matches 65; Conservative 34; Mismatches 116; Indels 136; Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NOMBER: 05/08/414,417B
FILING DATE: 31-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          920010.448C2
                                                     Sequence 68, Application US/08414417B Patent No. 5801005
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CLASSIFICATION: 424

ATTONNET; THOPRAMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 9200

REFERENCE/DOCKET NUMBER: 9200

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

(206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-6031 CONTROL SEQ ID NO: 68: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: amino acid; TOPOLOGY: linear US-08-414-4178-68
                                                                                                                                                                                                                                                                                                                                                                           98104-7092
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APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
TILLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: FIDDRY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,348A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY AATTONION: 424
Sequence 68, Application US/08486348A Patent No. 5846538 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFRENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPRAX: (206) 622-631
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
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NAME: Sharkey, Richard G
                                                                                                                                                                                                                                                                                                                                                                                Washington
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TOPOLOGY: linear
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US-08-468-545B-68

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TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROIEN FOR PREVENTION TITLE OF INVENTION: OR PREACHENT OF MALIGNANCIES IN WHICH THE HER-2/neu TITLE OF INVENTION: OR PREACHENT OF MALIGNANCIES IN WHICH THE HER-2/neu TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
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Best Local Similarity 18.2%; Pred. No. 11;
Matches 64; Conservative 34; Mismatches 117; Indels 136; Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
SOFTWARE: Floppy disk
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Nelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FLING DATE: OI-APPR-1996
CLASSIFICATION: 4424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C7
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
WUDER: AMINO ACID
                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-625-101-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 98104-7092
        SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214
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                                                                                                              APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | '| ::| || :| :| :| 387 SNTAPLQPEQLQVFETLEEITGYLSYLSAWPDSLPDSLPSVFQNLQVIRGRILHNGAYSLTLQ 446
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18.5%; Pred. No. 0.42;
tive 34; Mismatches 116; Indels 136; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 SRRIPYSRDRLPPFETETRAT----ILEDHPLLPECNTL------TMHNVSY---VR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GLPCS------VGFTLIQE------KCMH 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 585 VACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDD---KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535 IRGOECVEECRVLOGIPRE-----YVNARHCIPCHPECOPONGSVT---CFGPEADQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,545B
FILLING DATE: 06-JUN 1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:

NAME: Sharkey, Richard G.

NAME: Sharkey, Richard G.

NAME: Sharkey, Richard G.

REFERENCE/DOCKET NUMBER: 920010.448C5

REFERENCE/DOCKET NUMBER: 920010.448C5

TELECOMMUNICATION INFORMATION:

TELEFORMATION FOR SEQ ID NO: 68:

TELEFORMATION FOR SEQ ID NO: 68:

TELEFORMATION FOR SEQ ID NO: 68:

TELEFORMATION FOR SEQ ID NO: 68:

TELEFORMATION FOR SEQ ID NO: 68:

TELEFORMATION FOR SEQ ID NO: 68:

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TELEFORMATION FOR SEQ ID NO: 68:

TELEFORMATION FOR SEQ ID
Sequence 68, Application US/08468545B Patent No. 5876712 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XX: US
98104-7092
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7620-356-786-2 ; Sequence 2, Application US/08356786 ; Patent No. 5877305

RESULT 7 US-08-625-101-2 ; Sequence 2, Application US/08625101 ; Patent No. 5869445

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STATE: NEW YORK
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 19898
ADDRESSEE: GENERCOR INTERNATIONAL, INC.
STREET: 4 CAMBRIDGE PLACE
STREET: 1870 SOUTH WINTON ROAD
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHOD FOR THE TITLE OF INVENTION: PRODUCTION OF 1 WIMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  VASANTHA NAGRAJAN
WARK S. PAYNE
STEPHEN K. PICATAGGIO
RAMESCH V. NAIR
                     Sequence 11, Application US/08968563 Patent No. 6013494
                                                                                          CHARLES E. NAKAMURA
ANTHONY A. GATENBY
                                                                                                                                        LMY (KUANG-HUA) HSU
XICHARD D. LA REAU
                                                                                                                                                                                                       MARIA DIAZ-TORRES
DONALD E. TRIMBUR
                                                                                                                                                                                                                                                        REGORY M. WHITED
                                                                                                                                                                                      HARON L. HAYNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: GPD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
STREET: 10C
CITY: WILMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
US-08-968-563-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-968-563-11
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4.6%; Score 74; DB 2; Length 1255;
Best Local Similarity 18.2%; Pred. No. 11;
Matches 64; Conservative 34; Mismatches 117; Indels 136;
                                         APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: 18
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREFT: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 CARRTR-----RIMLRAVRIIAEETTAMLYSCRTERRRQQF----IRALLQ 279
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                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION 424
PRIOR PAPPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-356-786-2
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104 ANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFIWYRE 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.6%; Score 73; DB 3; Length 391; Best'Local Similarity 23.2%; Pred. No. 2.5; Matches 45; Conservative 21; Mismatches 58; Indels
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,601
FILING DATE: NOVEMBER 13, 1996
ATTORNEY AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERNEK/COCKET VNABER: CR-9982
TELECOMMUNICATION:
TELEPHONE: 302-892-8112
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RESULT

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| || || : 236 QSSC-HVMQQQCCQQL 250
                                                                                RESULT 11
5240838-5
;Patent No. 5240838
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; LENGTH: 664
5240838-5
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US-08-484-438-4
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                                              OV. .....164 .VVNTNMPKEVNFMSSVFMRGR-----HLIYLRLWYDG--HVGSVVPAMSFGYSALHCGIL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 ------ECNTLTMHNVSYVRGL-----PCSVGFTLIQEWVVPWDM--VLTREELVI 92
                                                               D. T. TVAXHIPKD-----FRGEGKDVDHKVLKALFHRPYFHV-SVIEDVA-GISI--CGAL 244
          --ET 196
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MERCHITELLY, CINZIA
APPLICANT: MERCHITELLY, CINZIA
APPLICANT: CARDELLY, LOTSA ERCOLI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A GENE
TITLE OF INVENTION: ENCODING A LOW MOLECULAR WEIGHT GLUTENIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 4.5%; Score 71; DB 2; Length 369; 1 Similarity 21.3%; Pred. No. 4; 29; Conservative 18; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 PFGMTLRPIRSR---LSRRIPYSRDRLPPFETETRATILEDHPLLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/991,300
FILING DATE: 16-DEC-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT MI 96/A 002663
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F:
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2264-0201-0X
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                             RESULT 10
US-08-991-300-2
; Sequence 2, Application US/08991300
; Sequence 59/3225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            703-413-3000
DD 180 SGANIATEV---AQEHWS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRKCMHVC--LCCANI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: prote#n
US-08-991-300-2
                                                                                                                              1:1 | 1 : 1
                                                                                                                                                                         Db. ...245 KNVVALGCGFVEGL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
ZIP: 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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468 ARRMESFAGEVTSHHPLFKVDSPARARDLDLETCSAYAGPKHLTANLYHG--SWTVPIDK 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MITSGVPFGWILRPIRSRLSRR-TPYSRDRLPPFETETRATILE------DHPLLPE 50
### APPLICANT: LEDBEDGER, ADRIANUS M.; MAAT, JAN; VERRIPS, CORNELLS
| TAPLICANT: LEDBEDGER, ADRIANUS M.; MAAT, JAN; VERRIPS, CORNELLS
| TILE OF INVENTION: REGULATORY SEQUENCES OF ALCOHOL OXIDASE
| (MOX) AND DITUDROXYACETONESYNTHASE (DAS) OF HANSENULA POLYMORPHA
| (MOX) AND DITUDROXYACETONESYNTHASE (DAS) OF HANSENULA POLYMORPHA
| CURRENT APPLICATION DATA:
| APPLICATION NUMBER: 05/07/587,555
| FILLING DATE: 24-SEP-1990
| APPLICATION NUMBER: 300,211
| FILLING DATE: 23-JAN-1989
| APPLICATION NUMBER: 759,315
| FILLING DATE: 26-JUL-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 19.1%; Pred. No. 9.5;
Matches 37; Conservative 24; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Plowman, Gregory D.
APPLICANT: Showah, Mohammed
APPLICANT: Shoyab, Mohammed
APPLICANT: Slegall, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CIITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08484438
Patent No. 5811098
Patent No. 5811098 5780031
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PRILICATION WORRER: USG/9(444.438
FILLIAN DAYS: 07-30K-1995
PROJECTION WORRER: USG/9(194.444)
PROMORED: 07-30K-1995
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PROMORED: 07-30K-1995
PROMORED: 07-30K-190K-1995
PROMORED: 07-30K-190K-1995
PROMOR
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69 VGFTLIQEWVVPWDMVLTREELVILRKCMH-----VCLCCANIDIMTSMMIHGYESW 120
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Sequence 8, Application US/0839000A
Sequence 8, Application US/0839000A
Sequence 8, Application Sequence
TILE OF INVENTION:
TILE OF INVENTION:
CONRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COUNTRY US.A.
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: US.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION:
AMB: MISTOCK, S. Leslie
CLASSIFICATION:
NAME: MISTOCK, S. Leslie
NAME: MISTOCK, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 1308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ALHCHCSSPGSLQCIAGGOVLASWFRMVVDGAMF-NQRFIWYREVVNYNM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.4%; Score 70.5; DB 2; Best Local Similarity 24.5%; Pred. No. 29; Matches 27; Conservative 20; Mismatches 46;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION NUMBER: 850-1092
ATTORNEYAGENT INFORMATION:
NAME: MASTOCK SILESIES
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 5624-230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-8864/9741
TELETAX: (6141 PENNIE
TELETAX: (6141 PENNIE
INFORMATION POR SEQ 1D NO: 2:
GENTERNEY CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 69
ELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1308 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-484-438-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Search completed: June 23, 2000, 10:04:33 Job time: 2838 sec
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                                                                                                                                                                                                                                           81 WDMVLTREELVILRKCMHVCLCCANIDIMTSMMIHGYE-SWALHCHCSSPGSLQCIAGGQ 139
                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                    140 VLASWFRMVVDG------AMFNQRFIWYREVVNYNMPKEVMF 175
                                                                                                                                                                                                                                                                                                                                           DB 2; Length 348;
                                                                                                                                                                                                           37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Budziak, Robert M.
APPLICANT: Shepard, H. Michael
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: HERZ EXTRACELLULAR DOMAIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: General
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSETWARE: WinPatin (Genentech)
                                                                                                                                                                     Query Match 4.4%; Score 70; DB 2
Best Local Similarity 20.9%; Pred. No. 4.8;
Matches 23; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lee, Wendy m
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 554C2D2
TELECOMMUNICATION INFORMATION:
THIRDHONE: 415/225_1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIEICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/355460

TELLING DATE: 13-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/048346
FILING DATE: 15-APR-1993
PRIOR APPLICATION NUMBER: 07/354319
APPLICATION NUMBER: 07/354319
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08422108
Patent No. 6015567
                                         : 348 amino acids
amino acid
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 348 amino acio
                                                                                            , MOLECULE TYPE:
US-08-390-000A-8
                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-422-108-1
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20 SRRIPYSRDRLPPFETETRAT----ILEDHPLLPECNTL------TMHNVSY---VR 63
                                                                                                              426 GLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVG 485
                                                                                                                                                                                                                                                99 VCLCCANIDIMISMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRWVVDGAMFNQRF 158
                                                                                                                                                                                                                                                                                            ----- 513
                                                                                                                                                                                                                                                                                                                               159 IWYREVVN-----YNMPKEVMFMSSVFMRGRHLIYLRIWYDGHVGSVVPAMSFGYSALHC 213
                                                                                                                                                                                                                                                                                                                                                              64 GLPCS------VGFTLIQE----WVVPWDMVLTREELVILR-----KCMH 98
                                       Gaps
                                       96;
Length 624;
                                       Indels
                                                                                                                                                                                                                                                                                          486 EGLACHQL------CARGHCWGPGPTQCVNCSQ------
4.4%; Score, 70; DB 3;
19.7%; Pred. No. 11;
tive 24; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                          214 GILNNIVVLCCSYCADLSEIRVRC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VACAHYKDPPFCVARC 579
  Query Match
Best Local Similarity 19.7%
Matches 52; Conservative
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June 23, 2000, 09:36:35; Search time 61.02 Seconds (without alignments) 282.484 Million cell updates/sec US-09-214-478-2 1594 1 MITSGVPFGMILRPIRSRLS.....RALLQHHRPILMHDYDSIPM 294 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Run on:

168808 Total number of hits satisfying chosen parameters:

168808 segs, 58629743 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR\_63:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	34K	E4 17K	E4 33K	protein	hypothetical prote	formate dehydrogen	hypothetical prote		hypothetical prote	hypothetical prote	opsin, rod - Pomat	NADH dehydrogenase	E2 protein - human	NADH dehydrogenase	hypothetical prote	probable respirato	pectate lyase (EC	NADH dehydrogenase	opsin, ultraviolet	NADH dehydrogenase	NADH dehydrogenase	dGTPase (EC 3.1.5.				hypothetical prote	probable membrane	hypothetical prote	heat shock protein
ΔI	Q4ADC2 S10867	04ADB2	Q4 ADM1	QOBE4	T32644	A70390	T24098	151200	T16796	T26242	S40688	B58851	836506	T11502	T30505	T35003	T05240	S01187	A48191	QXBO4M	T11411	A35993	T05131	T24487	S45424	T32277	865225	T23191	A40623
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Length	294	153	288	Ē	494	211	1603	354	456	562	352	459	378	459	530	642	374	446	354	459	459	502	528	373	458	303	321	895	196
% Query Match	100.0	20.8	11.7	5.6	5	5.4	5.1	5.1		•		5.0	4.9	6.4	4.9	4.9	4.8	4.8	4.8	4.	4.8	4.8	4.8	4.7	4.7	4.7	4.7	4.7	4.6
Score	1594	331	186.5	88.5	87	85.5	82	81.5	79.5	79.5	79	79	78	77.5	77.5	77.5	77	77	76.5	76.5		92	16	75.5	75.5	74.5	74.5	74.5	74
Result No.		4 M	4	ហ	ω	7	ω	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	ď	25	. 56	27	. 58	29	ဓ

protein-tyrosine k NADH dehydrogenase NADH dehydrogenase probable iron-sulf protein kinase A-r protein kinase A-r protein kinase A-r hypothetical prote glycerol-3-phospha	phospholipase C ho
A24571 114056 114056 125797 125797 200726 174104 A33931 541829 7111059 111149	T42440
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1235 4446 6004446 1339 1352 1352 1459 1459	1898
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47	72.5
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## ALIGNMENTS

`	RESULT	•		•
\	04ADC2		The second secon	•
	early E4		2.7	<b>~</b>
	C; Specie		The second secon	
	A; Note:			:5
	C;Date:	C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 04-Mar-1994		C
	C; Acces	lon: A03805	\$	, 1
	R; Herisa	e, J.; Rigolet, M.; Dupont de Dinechin, S.; Galibert, F.	the second secon	٠, ,
	Nucleic	Acids Res. 9, 4023-4042, 1961 Nucleotide segmence of adepovitue 2 DNA fragment encoding	for the carboxyl1	X
	A; Refere	A; Reference number: A93733; MUID:82059444	•	-
	A; Acces	A; Accession: A03805		€.
	A; Molecı		***	Ţ
	A; Resid	A; Residues: 1-294 <her></her>	The same of the state of the st	1
	A; Note: thi	s probable procesn was assigned by corretaining	מומר כו בהתכיבות ביות	Ş.,
	A; Map po	A; Map position: 92.6-95.2	A XI	3,
	C; Super	C; Superfamily: adenovirus early E4 34K protein		,
	C; Keywol	•		٠.
			*** *** *** *** *** *** *** *** *** **	ŧ.
	Query Match	Match 100.0%; Score 1594; DB 1; Length 294;		٠.
	Match	~~	0; Gaps 0;	
	Οÿ	1 MITSGVPFGMILRPIRSRLSRRIPYSRDRLPPFETETRATILEDHPLLPECNTLTMHNVS	MHNVS 60	
	i	-		
	QQ	l MTISGVPFGMTLRPIRSRLSRRIPISRDRLFFFFFFRATLLEDHFLLFECNIL		
	δλ	61 YVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRKCMHVCLCCANIDIMTSMAIHGYESW	120	1 -
	q	61 YVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRKCMHVCLCCANIDIMTSMMIHGYESW	120	10
	0y 1:	121 ALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFIMYREVVNYNMPKEVMFMSSVF	MSSVF 180	
	Db 1:	121 ALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFMSSVF	MSSVF 180	ż
	0y 1	181 MKGRHLIYLRLWYDGHVGSVVPAMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCAR	240	٠.
	Db 13	181 MRGRHLIYLRLWYDGHVGSVVPAMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCAR	RCCAR 240	
	0y 2	241 RTRRLMLRAVRIIAEETTAMLYSCRTERRRQGFIRALLOHHRPILMHDYDSTPM	294	
	Db 2	241 RIRRIMLRAVRIIAEETTAMLYSCRIERRRQQFIRALLQHHRPILMHDYDSTFPM	294	

early E4 34K protein - human adenovirus 12 C;Species: Mastadenovirus h12 (human adenovirus 12) C;Species: Pseb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999 C;Accession: S10867; S3952 R;Hogenkamp, T.; Esche, H.

billill	Mon Jun 26 09:10:37 2000	78-2.rpr Page 2	
it will	**Nuclear Acids Res. 18, 3065-3066, 1990		
e letter d		1 MITSGVPFGMILRPIRSRLSRRIPYSRDRLPPFEIETRAILEDHPLLPECNTLIMHNVS 61 IVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRRCMHVCLCCANIDIMTSMMIHGYESW	
		DD 61 YA 67 QY 121 ALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFIWYREVVNY 167	
i.		Db 67SPPVEQPQVGQPVAQQLDSDMNLSELPGEFINITDERLARQETVWNITPKNM 119	
	A.Accession: S33952 A.Status: preliminary A.Molecule type: DNA A.Molecule 179-7 (27, 230, 201, 201)	QY 168 NMPKEVMFMSVFMRGRHLIYLRLMYDG 195 :: ::   :               Db 120 SVTHDMMLFRASRGERTVYSVCWEGG 145	
	A; Mesiques: 1-17, CA; A50-241 ASENA A; Cross-references: EMBL:X73487; NID:g313361; PIDN:CAA51901.1; PID:g313386 C; Superfamily: adenovirus early E4 34K protein	RESULT 4	
	Query Match 53.9%; Score 858.5; DB 2; Length 291; Best Local Similarity 55.0%; Pred. No. 6.2e-73; Matches 149; Conservative 52; Mismatches 69; Indels 1; Gaps 1;	early E4 33K protein - mouse adenovirus 1 C:Species: Mastadenovirus musi (mouse adenovirus 1) A:Note: host Mus musculus (house mouse) C:Date: 30-Jun-1992 #secuence revision 30-Jun-1992 #text chance 04-Mar-1994	
	QY 21 RRIPYSRDRLPPFETETRAII-LEBHPLLPECNTLIMHNVSYVRGLPCSVGFTLIQEWVV 79	(.R. sarrian of true tradator of mounts.	7 1
	OY 140 VLASWFRMVVDGAMFNQRFIWTREVVNYNMPKEVWFMSSVFMRGRHLIYLRLWTDGHVGS 199 :    :      :        :		4
	QY 200 VVPAMSEGYSALHGGILNNIVVLCCSYCADLSEIRVRCCARRTRRIMLRAVRIIAEETTA 259 190 ALEKVSFGWSAFNYGILNNMLVLCCDYCKDLSEIRMRCWPRRTRLIMLKVVQVIAENTVR 249	Query Match 11.7%; Score 186.5; DB 1; Length 288; Best Local Similarity 24.8%; Pred. No. 4.7e-10; Matches 68; Conservative 43; Mismatches 120; Indels 43; Gaps 11;	
	QY 260 MINSCRTERRROGFIRALLOHHRPILMHDYD 290  DD 250 PLKHSRHERYRQQLLKGLIMHHRAILFCDYN 280	IOEWVVPWDMVLTREBLVILRK 95	學的原
	en	OY 96 CMHVCLCCANIDIMISMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFR 146	
		0 4	1
	*text_change 12-Apr-1996; Galibert, F.		*
• (	A; Tille: Nucleotiue sequence of adenovirus 2 DNA fragment encoding for the carboxylic re A; Reference number: A93733; MUID:82059444 A; Racession: A03804 A; Rolecule type: DNA A; Residiues: 1-153 chre.		
į	A; Note: these probable proteins and the introns in the coding regions were assigned by c C; Genetics: A; Map position: 91.8-95.2		
÷	A;Introns: 61/3 C;Superfamily: adenovirus early B4 17K protein C;Keywords: early protein F;56-153/Product: early E4 10K protein *status predicted <tpp></tpp>	ext_change 23-Aug-1997	, , , , ,
	Match 20.8%; Score 331; DB 1; Leng ocal Similarity 38.5%; Pred. No. 7.2e-24; s 80; Conservative 10; Mismatches 42; In I.MITSGVPFGWILRPIRSRLSRRTPYSRDRLPPFETETRATILEDHPL	R.Bankler, A.T.: Deininger. P.L.; Farrell, P.J.; Barrell, B.G. Mol. Biol. Med. 1, 21-45, 1983 A.Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi. A.Reference number: A93065; MUID:85035713 A.Accession: C93065 A.Molecule type: DNA A.Residues: 1-191 - (BAN)	,

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C;Species: Aquifex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A70390
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;...
                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:AE000720; NID:92983529; PIDN:AAC07109.1; PID:92983534; GB:AE00
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4
A;Introns: 18/1; 57/3; 75/2; 120/1; 168/2; 194/1; 258/1; 302/2; 348/3; 392/3; 442/1;
                                                                                                                                                                                                                  Nature 392, 353-358, 1998
Aritle: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. Areference number: A70300; MUID:98196666
A; Accession: A70390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL:277134; PIDN:CAB00874.1; GSPDB:GN00022; CESP:R09H10.5
:e: clone R09H10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cipate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
Cipate: 17-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
Cipate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
Cipate: 17-0ct-1999 #sequence 15-0ct-1999 #text_change 15-0ct-1999
Sibate: 15-0ct-1999 #sequence 15-0ct-1999 #text_change 15-0ct-1999 #text_change 15-0ct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 GMTLRPIRSRLSRRIPYSRDRLPPFETETRATILEDHPLLPECNTLTMHNVSYV----R 63
                                                                                              formate dehydrogenase (EC 1.2.1.2) gamma chain - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A70390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 WVVFLSAIVFFLTGILMMPPENFSMGLVRWSVVIHEITFIIAGAFTIIHIYMATVGVPGS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: fdoI
C;Superfamily: formate dehydrogenase gamma chain
C;Keywords: heterotrimer; NAD; oxidoreductase; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein R09H10.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
5.1%; Score 82; DB 2;
Best Local Similarity 21.9%; Pred. No. 17;
Matches 44; Conservative 29; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 85.5; DB 1;
Pred. No. 0.95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1603 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVCLCCANIDIMISMMI-----HGYESWALHCH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 LOCIAGGOVLASWFRMVVDGAMFNQRFIWYREVV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : : ||:| |:|
184 IMGMIGGKVSATW-----AKFHHP-KWYREVV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 GLPCSVGFTLIQEWVVPW--DMVLTREELVILRKC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 23.4%;
Matches, 36; Conservative 20
| | :: ||:
249 ESYKTIWMFWCRS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source:
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A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A07994, MUDI:084270667
A;Contents: annotation; protein coding region
C;Superfamily: human herpesvirus 4 BHRF1 protein
C;Reywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CMHVCLCCANIDIMTS----MAIHG-----YESWALHCHCSSFGSLQCIAGGQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 NILYLFILACLDILVELCFMLIFPASLVWDYFRVELLYTCWHFYIKYVS-----TVGQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 VLASWERMVVDGAMENQRFIWYREVVNYNMPKEVMFMS-----SVFWRGRHLIYLRLWYD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 VLIAASTLLIVAASFERYICSLKSSIOFSPORRFLFISIVGACALFMKGSVFFELEL--- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EINDICAEDP---PQADAFRMILIVIIGTVVCSLGI-----VLNTFLLLSLRRLDVFRS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETRATILEDHPLLPECNTLTMHNVSYVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRK 95
                                                                                                                                                                                                                                                                                                                                                                                                                          105 N-----IDIMTSMMI---HGYESWALHCHCSSPGSLQCIAGGQVLASWFRAVVDGAMFN 155
                                                                                                                                                                                                                                                                                                                                              59 VS------YVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRKCMHVC--LCCA 104
                                                                                                                                                                                                                                                                                                                                                                                      .----CMHACRILCCN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GG-----WSTLIEDNIPGS 161
                                                                                                                                                                                                                                                                                            24 TLHPVLELAARETPL---RLSPEDT----VVLRYHVLLEBIIERNSETFTETWNRFITHT 76
                                                                                                                                                                                                                                                                       --NTLIMHN 58
                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.5%; Score 87; DB 2; Length 494; Best Local Similarity 20.2%; Pred. No. 1.7; Matches 51; Conservative 40; Mismatches 96; Indels
                                                                                                                                                                                       Length 191;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                77 EHVDLDFNSVFLEIFHRGDP-SLGRAL--AWMA-W------
                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                         11 TLRPTRSRLSRRTPYSRDRLPPFETETRATILEDHPLLPEC--
                                                                                                                                                                                               DB 1;
                                                                                                                                                                                           5.6%; Score 88.5; DB
illarity 23.3%; Pred. No. 0.45;
Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 QSTPXYVVDLSVRGMLEASEGLDGW-IHQQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 QRFIWYREVVNYNWPKEVMFMSSVFMRGRH 185
                                                                                                                                                                                               Ouery Match
Best Local Similarity
Matches 49; Conserv
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63;

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255 EE-TTAMLYSCRT 266

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Oy 220 VVLCC 224  Db 319 TTLCC 323  RESULT 10  T16796  hypothetical protein T04A6.3 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Acte: 20.50p-1999 #sequence_revision 20-Sep-1999	.6. 0335; PIDN:. 0/3; 374/1; 5tein T04A6 Length 456; Indels 12 PHPLLPECNTLI I.SMLP-CGT - I.SMLP-	Db 172 VNLPCEKQIFAKATHLITZRIMYDGHVGSVVPAMARGYSALHGGILNNI 219   1
OY 64 GLPCSVGFTLIQEWVVPWDMVLTREELVILRCCMHVCLCCANIDIMT 110  Db 1029 TSGCKYEYIMNGEYTCQSAGDTFTMETTITTNEVTIMRTORAYCSDLIGCINGGIMLGGN 1088  QY 111 SMMIHGYESWALHGHCSSPGSLOCIAGGVLASWFRAWYDGAMFNQRFIW 160  Db 1089 CQCVNGYTSLHCEVPTCQNGGSVVDFKCQCPSIYDGDSCQYTTCNTW 1135  QY 161 YREVYNYNMPKEVMFMSSVFM 181  Db 1136NFVETHDPREYNFQQIVFV 1154	Sep-1999  ceptor differentiatic  36188; EMBL:L04692; N  3ducin from Xenopus 1  214735  tein; lipoprotein; p	Duery Match  S.1%; Score 81.5; DB 1; Length 354;  Best Local Similarity 20.0%; Pred. No. 3.9;  Garbed File Conservative 33; Mismatches 94; Indels 117; Gaps 13;  S.07PEG FILEPTRERIESTRIPYSEDELPETRATILEDHPLIPECHILTHRNV 60  5.1 GLPINFWILEVITQHEKTPYSEDELPETRATILEDHPLIPECHILTHRNV 60  5.1 GLPINFWILEVITQHEKTPYSEDELFRATILEDHPLIPECHILTHRNV 60  5.1 GLPINFWILEVITQHEKTPYSEDELFRATILEDHPLIPECHILTHRNV 60  5.1 GLPINFWILEVITQHEKTPYSEDELFRATILEDHPLIPECHILTHRNV 60  5.2 GLPINFWILEVITQHEKTPYSEDELFRATILEDHPLIPECHILTHRNV 60  5.3 GLPINFWILEVITQHEKTPYSEDELFRATILEDHPLIPECHILTHRNV 60  1.1

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A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Superfamily: NADH dehydrogenase (upiquinone) chain (NAD; oxidative phosphorylatio
C; Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 07-Dec-1999 C; Accession: B58851 B58851 J. Wol. B58851 J. Wol. B58851 J. Wol. B58851 J. Wol. B58851 J. Wol. B58851 J. Wol. B58851 J. Wol. B58851 J. Wol. B58851 J. Wol. B58851 J. Wol. B58851 J. Wol. B58851 J. Wol. B58851 J. Wolecule type: DNA A; Accession: B58851 J. Wolecule type: DNA A; Accession: B58851 J. Wolecule type: DNA A; Accession: B58851 J. Wolecule type: DNA A; Cross-references: GB:X61145; NID:g12772; PIDN:CAA43448.1; PID:g12780 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sisting 1978

Sisting 1978

E2 protein - human papillomavirus type 30

C. Species: human papillomavirus type 30

C. Species: human papillomavirus type 30

C. Species: human papillomavirus type 30

C. Scession: Sisting 1993

Submitted to the EMBL Data Library, August 1993

Submitted to the EMBL Data Library, August 1993

Submitted to the EMBL Data Library, August 1993

A; Reference number: Sisting 0f human papillomavirus types.

A; Reference number: Sisting 0f human papillomavirus types.

A; Residues: 1.378 ADEL

A; Residues: L'378 ADEL

A; Residues: EMBL: X74474; NID: 9396973; PIDN: CAAS2546.1; PID: 9396977

A; Cross-references: EMBL: X74474; NID: 9396977

C; Superfamily: papillomavirus E2 protein

C; Superfamily: papillomavirus E2 protein; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 NY-----NMPKEVMFMSSVFMRGRHLIYLRLMYDGHVGSVVPAMSFGYSA---LHCGI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 ---HGYESWALHCHCSS---PGSLQCI-AGGOVLASWFRMVVDGAMFN--ORFIWYREVY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 KTEYKVEEWILKDVCENNWHTAPKQCFKKSGKRIEVWF----DGKKDNRTEYVVW--QWV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 IQEWVVPWDMYLTREELVILRK-----115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 FCLANSNYERIHSRTMILPGGLQVFL--PLMASWWLLA------SLTNLALP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 K-----EUMEMSSVF------MRGRHLIYLRLW-------YDGHVGSVVPAM 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 PIINLIGELLVVMSVFSWSNPTILLMGTNIVITALYSLYMLIMTORGKHTHHINNITPSF 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 WDMVLTR------BELVILRKCMHVCLCCANIDIMTS------MMIHGYESWAL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HCHCSS------PGSLQCIAGGOVLASWFRMVVDGAMFNORFIWYREVVNYNMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 WGMINTSSICLRQTDLKSLIAYSSVSHMALVIAAILIQTPWSYMGATALMIAHGLTSSML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.9%; Score 78; DB 2; Length 378; Best Local Similarity 21.6%; Pred. No. 8.9; Matches 50; Conservative 27; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 459;
8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 19.5%; pred. No. 8.8;
Matches 37; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431 TREHALMALH 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 SFGYS--ALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
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A, Residues: 1-352 <ARC.
A, Molecule type: MRNA
A, Residues: 1-352 <ARC.
A, Cross-references: EMBL: X62405, NID: 9433817; PIDN: CRA44275.1; PID: 9433818
A, Cross-references: EMBL: X62405, NID: 9433817; PIDN: CRA44275.1; PID: 9433818
A, Cross-references: EMBL: X62405
C; Reywords: Chromoprofesin: epe; G protein-coupled.receptor; glycoprotein; lipoprotein; C; Reywords: Chromoprofesin: epe; G protein-coupled.receptor; glycoprotein; lipoprotein; E; 74.96, Nomain: transmembrane #status predicted <TM3>
F; 14.94, Opomain: transmembrane #status predicted <TM4>
F; 230.-2307, Domain: transmembrane #status predicted <TM5>
F; 230.-2307, Domain: transmembrane #status predicted <TM5>
F; 286.-309, Domain: transmembrane #status predicted <TM7>
F; 286.-309, Domain: transmembrane #status predicted <TM7>
F; 286.-309, Domain: transmembrane #status predicted <TM7>
F; 286.-309, Domain: transmembrane #status predicted <TM7>
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F; 286.-309, Domain: transmembrane #status predicted <TM7>
F; 286.-309, Domain: transmembrane #status predicted <TM7>
F; 286.-309, Domain: transmembrane #status predicted <TM7>
F; 286.-309, Domain: transmembrane #status predicted <TM6
F; 296, Palnding site: retinal (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Pomatoschistus minutus) compared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                             6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------LWX------DGHVGSVVPAMSFGYSALHCGILNNIVVLCCS--- 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 SMHGYEVIGRIGCNVEGFFATIGGE-IALWSLVVLAVERWVV-----VCKPISNFRFTEN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 MMIHGYE-SWALHCHCSSPGSLQCIAGGQVLASWFRMVVDG------AMFNQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 HAIMGVAFSWIMAATCAVP------PLVGWSRYIPEGMQCSCGVDYYTRAEGFNNE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 TMHNVSYVRGLPCSV-GF--TLIQEWVVPWDMVLTREELVILRRCMHVCLCCANIDIMIS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                psin, rod - Pomatoschistus minutus
;psetse: Pomatoschistus minutus
;pate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
;Accession: $40688
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                                                                                                                                                                                                                                                                                                                                                        65 SSKRISALIEGLEVIQVLCLIAAFFLVFASAAMIYGIHTWSKYLV---WPWFPVMLSSIL 121
                                                                                                                                                                                                                                                                                                 . 135 -----IAGG----QVL---ASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFMSSVF 180
                                                                                                                                                                                                                                       6 CCCCSSKDAAITIGIWSLVYALASLLLFGWQTGVLN-HCRVVTWAQSNLQCEWDCPCVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98;
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19.9%; Pred. No. 6.6;
tive 31; Mismatches 76; Indels
                                                                            Length 562;
                                                                                                                                                                                          100 CLCCANID-----SPGSLQC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 AT---LAYCIMWWGGDVRSYWLAIT------ILEIIVVFINIYC 156
                                                                                                                                                                                                                                                                                                                                                                                                                     · 181 MRGRHLIYLRLWYDGHVGSVVPAMSFGYSALHCGILNNIVVLCCSYC 227
                                                                                                                                      48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiArcher, S.N.; Lythgoe, J.N.; Hall, L. 19-25, 1992 Proc. R. Soc. Lond. B Blol. Sci. 248, 19-25, 1992 Aritile: Rod opsin cDNA sequence from the sand goby A; Reference number: $40688; MUID:92396703 A; Accession: $40688.
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                                                                               5.0%; Score 79.5; DB 2;
23.4%; Pred. No. 9.8;
tive 25; Mismatches 48;
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Best Local Similarity 19.9
Matches 51; Conservative
                                                                                           5.0%
Best Local Similarity 23.4%
Matches 39; Conservative
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RESULT 15

RESULT 15

RESULT 15

C. Species: mitochondrion Canis lupus familiaris (dog)
C. Species: mitochondrion Canis lupus familiaris (dog)
C. Species: mitochondrion Canis lupus familiaris (dog)
C. Species: mitochondrion Canis lupus familiaris (dog)
C. Species: mitochondrion Canis lupus familiaris (dog)
C. Species: mitochondrion Canis lupus familiaris (dog)
C. Species: mitochondrion Canis lupus familiaris (dog)
C. Statin, K. S. Lee, S. E. Jeong H. W. Ha, J. H.
ANDICESTON: TISO
C. M. M. M. C. Complete nucleotide sequence of the domestic dog (Canis familiaris) mitochondrion
A. Residues: preliminary: translated from GB/EMBL/DDBJ
A. Residues: 1-459 KIMA
A. Residues: 1-459 KIMA
C. Genetics: EMBL: U96639; NID: 94154170; PID: 94154180; PIDN: AAD04772.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Nove: ND4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 TILEDHPLLPECNTLTMHNVSYVRGLPCSVGFTLIQEWVVP----WDMVLTREELVILRK 95
190 -NESI-----YCPD------SVSSTLRSNVSPVETVVEXNTYQTPT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 TIMGSLPLIVA-----LITIHNPMGSLNFLMIQYMIQPLPNSWSNIF---
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Best Local Similarity 24.1%; Fred. No. 12; Matches 26; Conservative 14; Mismatches
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Search completed: June 23, 2000, 10:05:43 Job time: 1748 sec

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*				-		73.5 4.6 606
	Copyright	GenCore ht (c) 1993	199	version 4.5 - 2000 Compugen	Ltd.	
OM protein - prot	tein search,		using	sw model		73 4.6 504
Run on:	June 23,	2000,	10:	10:03:39 ; Search time (without 640.012 M	ne 13.99 Seconds rt alignments) Million cell updates/sec	2 /2.5 4.5 4 72.5 4.5 5 72 4.5
Title: Perfect score: Sequence:	US-09-21 1594 1 MTTSGV	-09-214-478-2 94 MITSGVPFGMILRPIRSRLS	2 RPTF	:	. RALLQHHRPILMHDYDSTPM 294	
Scoring table:	BLOSUM62 Gapop 10.0	-	Gapext	t 0.5		SULT 1 34_ADE02
Searched:	83857 86	seqs, 30454973	454	73 residues		E434_ADE02 STANDAR
rotal number of	hits	satisfying		chosen parameters:	83857	
Minimum DB seq Maximum DB seq	length: 0 length: 1	1000000		·	-	DE EARLY E4 34 KD PROTEIN. OS Human adenovirus type 2.
Post-processing	: Minimum Listing	Match first	9 to	summaries		Viruses; dsDNA Viruses; [1] SEQUENCE FROM N.A.
Database :	SwissProt_38:*	t_38:*				
ed. ore	No. is the n greater than s derived by	umber or ec	of r	results predicted by chance to hat to the score of the result bein of the total score distribution.	chance to have a result being printed, stribution.	RT "Nucleotide sequence of a RT carboxylld region of the Nucleic Acids Res. 9:4023 CC -!- MISCELLANEOUS: FOUND
!	d			SUMMARIES		
Result No. Score	sery atch	Length DB		ព	Description	
<b>.</b>	0.00	94	1		human	
•	62.1	292		E434_ADE09 E434_ADE12	human	
~	4 4 6 4 6 6 6 6	257		E434_ADE40	uman a	
• • • •	15.0	259		E434_ADECT	p87568 canine aden Q96690 canine aden	
	15.7	265		E434_ADECC E434_ADEM1	anine ouse a	Early proteings 2
	7.00	643 191		UROM BOVIN EAR EBV	P48733 bos taurus P03182 epstein-bar	
	100 100	354 254 254		OPSD_XENLA OPSD_LIMBE OPSD_DOMMI	P29403 Xenopus Lac 042427 limnocottus P35403 pomatoschis	Query Match 100 Best Local Similarity 100
	0.00	354		OPSD_ZEUFA	042604 zeus faber p24975 balaenopter	Matches 294; Conscitation
	0.00	378		VEZ_HPV30	P36790 human papil	
	44.	200 100 100 100		NU4M_CANFA OPSD_BAIMU OPST_PRAPE	042300 batrachocot p35359 brachydanio	⊢ ;
	4.4.4 2.00	4 5 5 4 4 5 5 6 4 5 6 6		OFSU_BRANE NU4M_BOVIN NI4M FFICA	P03910 bos taurus P48916 felis silve	Oy 61 YVRGLECSVGF1LLTCENV
	υ εν α ο εν α	50 50 50 80 50 80		NTG1_MUSCO DGTP_ECOLI	P48057 mus cookii. P15723 escherichia	
	44	504 518		DGTP_ESCFE PEL1_YEAST	Q59435 escherichia P25578 saccharomyc	
		3458		ALG3_YEAST OPSD_MYRBE UMG8_ECOLT	P79798 myripristis P28697 escherichia	181
	44.	350	4	ILBA GORGO	p55919 gorilla gor p04626 homo sapien	DD 181 MRGRHLIYLRLWYDGHVG
33 73.5	1001 144 1000	446	4 ~ ~ ~	NUGA DROYA YKGF ECOLI KRAA RAT	p07707 drosophila p77536 escherichia p14056 rattus norv	Qy 241 RTRELMERAVRITAEETT
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P10398 homo sapien
019004 sus scrofa
042452 parecotus
062796 trichechus
000055 saccharomyc
059827 shigella bo
P17439 mus musculu
P30992 canis famil
P41298 balaenopter
078755 ovis aries
042294 abyssocottu
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Dupont de Dinechin S., Galibert F.; adenovirus 2 DNA fragment encoding for the e fiber protein and the entire E4 region."; 23-4042(1981) D IN ASSOCIATION WITH E1B 55 KD PROTEIN. TO THE ADENOVIRUS E4 30 TO 34 KD PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                    no RNA stage; Adenoviridae; Maskadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAMLYSCRIERRROOFIRALLOHHRPILMHDYDSTPM 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.0%; Score 1594; DB 1; Length 294; 00.0%; Pred. No. 6.3e-148; e 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                   eated)
st sequence update)
st annotation update)
                                                                                                                                                                                                                                                                                  PRT; 294 AA.
                                                                                                                                                                                                        ALIGNMENTS
      KRAA_HUMAN
KRAA_PIG
OPSD_PARKN
OPSD_PARKN
OPSD_PARKN
CPD1_YEAST
CGP1_YEAST
CGP2_SHIBO
GLCM_OOTSE
C5AR_CANFA
NU4M_BALMU
NU4M_BALMU
NU4M_SHEEP
OPSD_ABYKO
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精点 (資本) (日本)

EARLY E4 34 KD PROTEIN. Human adenovirus type 9.

SEQUENCE FROM N.A. MEDLINE; 96327849.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 PWDMVLTREELVILRRCMHVCLCCANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 VLASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFWSSVFWRGRHLIYLRLWYDGHVGS 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEDLINE; 94076430.
Sprengel J., Schmitz B., Heuss-Neitzel D., Zock C., Doerfler W.;
"Nucleotide sequence of human adenovirus type 12 DNA: comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
EARLY E4 30 KD PROTEEN.
Human adenovirus type 40.
                                                                                                                                                                     Hogenkamp I., Esche H.;
"NotLeotide sequence of the right 10% of adenovirus type 12 DNA encoding the entire region E4.";
Nucleic Acids Res. 18:3065-3066(1990).
-I SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KD PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-DUGAN;
MEDLINE; 9408748.
Davison A.J., Telford E.A., Watson M.S., McBride K., Mautner V.;
"The DNA sequence of adenovirus type 40.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.9%; Score 874.5; DB 1; Length 291; 55.7%; Pred. No. 6.5e-78; Idve 52; Mismatches 67; Indels 1.
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CD1A07D37FBB5E96 CRC64; \
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291 AA; 34383 MW;
                                                                             functional analysis.";
J. Virol. 68:379-389(1994).
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EMBL; X51800; CABS7854.1;
PIR; S33952; S33952.
PIR; S10867; S10867.
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Best Local Similarity 55.77
Matches 151; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                 SEQUENCE
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Q64865;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGE 12 STANDARD; PRT; 291 AA.
P36710;
01-70N-1994 (Rel. 29, Created)
01-70N-1994 (Rel. 29, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
EARLY E4 34 KD PROTEIN.
Human adenovirus type 12.
Truses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                  Javier R., Shenk T.;
Javier R., Shenk T.;
Mammary tumors induced by human adenovirus type 9: a role for the viral early region 4 gene.";
Breast Cancer Res. Treat. 39:57-67(1996).
-1 SIMHIGHRITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KD PROTEIN
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 VPAMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCARRIRRLMLRAVRIIAEET -- T
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241 RTRELMELRAVRIIAEETTAMENSCRIERRRQOFIRALEQHHRPILMHDYDSTPM 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.1%; Score 990; DB 1; Length 292; 63.7%; Pred. No. 3.8e-89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 AA; 34082 MW; 1F0815EDEF2A2A1E CRC64;
                                                                                                                                                                   , Last annotation update)
                                                                                                  292 AA
                                                                                                                                                    Last sequence update)
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                                                                                                PRT;
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EMBL; S82508; AAB37508.1; -.

SEQUENCE Early

Query Match 62.19 Best Local Similarity 63.77 Matches 174; Conservative

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RESULT 3
E434\_ADE12
D E434\_A
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RP SEQUEN

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-!- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 82059444.

Herisse J., Rigolet M., Dupont de Dinechin S., Galibert F.;

Herisse J., Rigolet M., Dupont de Dinechin S., Galibert F.;

Herisse J., Rigolet M., Dupont de Dinechin S., Galibert F.;

Nucleotide sequence of adenovirus 2 DNA fragment encoding for the

"Nucleotide sequence of the fiber protein and the entire E4 region.";

Carboxylic region of the fiber protein and the introns IN THE

Nucleic Acids Res. 9:4023-4042(1981)

Nucleic Acids Res. 9:4023-4042(1981)

-1- MISCELLANEOUS: THESE PROBABLE PROTEINS AND THE INTRON SPLICING.

CODING REGIONS WERE ASSIGNED BY CORRELATING EM DATA, S1 DIGESTION

CODING REGIONS WERE ASSIGNED BY CORRELATING EM DATA, S1 DIGESTION

STUDIES, AND THE CONSENSUS SEQUENCES FOR INTRON SPLICING.
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SEQUENCE 257 AA;
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P03238;
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-21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
PROBABLE EARLY E4 17 KD PROTEIN [CONTAINS: E4
Human adenovirus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; J01917; -; NOT_ANNOTATED_CDS. PIR; A03804; Q4ADB2.
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llarity 50.2%;
Conservative '
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Pred. No. 1.4e-61;
7; Mismatches 77; Indels
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Matches 70
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Submitted (NOV-1996) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
EARLY E4 30 KD PROTEIN.
Canine adenovirus type 2 (strain Toronto A 26-61).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                     Early protein. SEQUENCE 259
                                                                                                                                                                                                                                              EMBL; U77082; AAB38735.1; -.
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                                                                                                    NORFIWYREVVNYNMPKEVMEMSSVFMRGRHLIYLRLWY----
                                                                    KCMHVCLCCANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMF 154
NKKYMWYREFVNSSRPDEINYVGSIIFRNTHYIYFRLSFFRTVHKACMEA¶KRCINPELG
                                                                                                                                                                    Similarity
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56
153 AA;
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                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                      AA;
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153
17404
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                                                                                                                                                                                                                      30014 MW;
                                                   -----QTWRVHCHCSNSLSLQCMASKHVVQKVIEDFIKGGAM
                                                                                                                                                                    15.9%;
                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ databases. TO THE ADENOVIRUS E4 30 TO 34 KD PROTEIN
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                                                                                                                                                           47;
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Pred. No. 2.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLY 17 KD PROTEIN EARLY 10 KD PROTEIN; 1B3A657DAD8557CC (
                                                                                                                                                        Score 253.5; DB 1;
Pred. No. 1.5e-17;
7; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                        9C966CA011C2A745 CRC64;
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                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
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                             -----DGHVG 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 ONTITMENVSTYRGLP -- CSVGFTLIQEWVVPWDMVLTREELVI------LRKCM 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 CNAETTSHVTAVVRAPIFCNC-FALCLEIPILWDDLLYRHEKLLFGGFTCNGGAELILNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 -- KAEERRQTALKQAMMYGR . 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 SALHCGILNNIVVLCCSYCADLSEIRVRCCARRTRRLMLRAVR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 YLWYREFVNSSRPDEINYVGSIMFRNIHYIYFRLSFFSTVHQACMLAIQRCISPELGVVF
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"Complete DNA sequence of canine adenovirus type 1.";
J. Gen. Virol. 78:873-878(1997).
-i- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 31 TO 34 KD PROTEIN
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Viruses; dsDNA viruses, no RNA stage; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLY E4 31 KD PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168
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                                                                                                                                                                                                                                                                                                                                                                                            KSTY----NYWLVLKCKSCSLQNYCALKSCAFWVRSIIDRVLREVEKIPVVLHRTTS---
                                                                                                                                                                                                                                                                                                                                             SCRTERRROOFIRALLOHHR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCCLADA------QMWQVHCHCSDSLSLQCLSATQVLKEFLEEFVMGGFVNKK 116
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(Rel. 37, Last sequence update)
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(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 252.5; DB 1;
Pred. No. 2e-17;
                                                                                                                     PRT;
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STANDARD; PRT; Zo5 F...

C P23125;

T 01-NOV-1991 (Rel. 20, Created)

JT 01-NOV-1995 (Rel. 32, Last sequence update)

JT 15-DEC-1998 (Rel. 37, Last annotation update)

DE PROBABLE EARLY E4 33 KD PROTEIN (ORF A/B PROT

PROBABLE EARLY E4 33 KD PROTEIN (ORF A/B PROT

JEAN Adenovirus type 1 (MAV-1).
SEQUENCE FROM N.A.

SEQUENCE, 91082417.

Ball A.O., Beard C.W., Villega:

"Early region 4 sequence and b:

mouse adenovirus type 1.";

Virology 180:257-265(1991).
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                          177 KSTY----NYWLVLKCKSCSLQNYCALKSCAFWVRSIIDRVLREVEKIPVVLHRTTS---
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Canine adenovirus type 1 (strain CLL)
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Dragulev B.P., Sir
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                                                                                                                                                                                                                                                                                                                                              --KAEERRQTALKQAMMYGR
                                                                                                                                                                                                                                                                                                                                                                              SCRTERRRQQFIRALLQHHR 282
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) to the EMBL/GenBank/DDBJ databases
                               Villegas P., Spindler K.R.; ce and biological comparison
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                                                                                                                    RNA stage; Adenoviridae; Mastadenovirus
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Pred. No. 3.1
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ber genomic regions
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01-FEB-1996
15-FEB-2000
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Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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                                                                                                                                      SEQUENCE FROM N.A. TISSUE-KIDNEY; MEDLINE; 95143938.
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'SPLICED FROM THE SAME PRIMARY TRANSCRIPT.
SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KD PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CMHYCLCCANIDIMTSM--MIHGYESWALHCHCSSPGS-----LQCIAGGQYLASWFR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPLTMS -- ATLSRMDCCVGLPHCMGWLPSPVGAVAFVMEGALPIPWSYYLNSYDKHVLQQ
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6 (Rel. 33, Last sequence update)
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0 (Rel. 39, Last nnotation update)
PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP).
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Pred. No. 5.8e-11;
3; Mismatches 120
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PROSITE; PS00682; ZP_DOMAIN; 1.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS00022; EGF_1; FALSE_NEG
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01187; EGF_CA; 2.
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CARBOHYD
SEQUENCE
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C--VPVLHCNTAAPMWLNGTHPSSDEGIVNRVACAHWSGDCCLWDA---PIQVKACA
                                                                                 VCVDPCQVHRILDEYWRSTEYGSG----YICDVSLGG-----WYRFVGQAGVRLPET
                                                                                                                             MYVDGAMFNQRFIWYREVVNYNMPKEVMFMSSVFMRGRHLIYLRLWYD--GHVGSVVPAM 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M17416; AAA45873.1; -.
EMBL; V01555; -; NOT_ANNOTATED_CDS.
EMBL; M17293; AAA45875.1; -.
EMBL; A22899; CAA01838.1; -.
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Baer R.; Bankler A.T., Biggin M.D., Deininger P.L., Faller.

Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,

ZTUTINELLES., Barrell B.G.;

C"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";

Nature-310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                               Early
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MEDILINE; 87284169.

Pfitzher A.J., Tsai E.C., Strominger J.L., Speck S.H.;

"Isolation and characterization of cDNA clones corresponding to
"Isolation the BamHI H and F regions of the Epstein-Barr o
                                      105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- MISCELLANEOUS: EA-R IS PART OF THE RESTRICTED EA-COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of an Epstein-Barr virus early gene encoding a second component of the restricted early antigen complex."; virology 160:151-161(1987).
-:- FUNCTION: INHIBITS APOPTOSIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
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15-JUL-1998 (Rel. 36,
EARLY ANTIGEN PROTEIN
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                                                            EHVDLDFNSVFLEIFHRGDP-SLGRAL--AWMA-W------
                                                                                                                     TLHPVLELAARETPL---RLSPEDT----VVLRYHVLLEEIIERNSETFTETWNRFITHT 76
                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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GCRDB; GCR_0487; -.

GCRDB; GCR_0497; -.

GCRDB; GCR_0972; -.

PRINTS; PR00238; OPSIN.

PROSITE; PR00237; G_PROTEIN_RECEPTOR; 1.

PROSITE; PS00237; OPSIN; 1.

PROSITE; PS00238; OPSIN; 1.

PROSITE; PS00238; OPSIN; 1.

PRAM; PF00001; Trunl; 1.

Photoreceptor; Retinal protein; Transmen
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ENBL; U238c.
TR; S31473; S
 Phosphorylation; Lipoprotein; p
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VISION IN DIM LIGHT.

1- PIM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR
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01-APR-1993
15-JUL-1999
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"Characterization of the Xenopus rhodopsin gene.";
J. Biol. Chem. 271:3119-3186(1995)
-1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
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n; Palmitate; G-p
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1 (POTENTIAL).
CYTOPLASMIC.
2 (POTENTIAL).
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OF AN APOPROTEIN, OPSIN, COVALE
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PHOTORECEPTOR CELLS WHICH MEDIATES
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                                                                                                                                                                             Limnocottus bergianus.
Limnocottus bergianus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Eukaryota; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Scorpaeniformes; Cottoidei; Abyssocottidae; Limnocottus.
"Molecular evolution of the cottoid fish endemic to Lake Baikal deduced from nuclear DNA evidence.";
deduced from nuclear DNA evidence.";
deol. Phylogenet. Evol. #415-422(1997).
HOL. Phylogenet. Evol. #415-422(1997).
HEDIATE VISIAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT HEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                           SEQUENCE FROM N.A.
MEDLINE: 98086781.
Hunt D.M., Fitzgibbon J., Slobodyanyuk S.J.,
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                                                                                               Dulai K.S.;
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P35403;
P35403;
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Score 79; Pred. No.

DB 1;

Length 289; Indels

22;

Mismatches

54;

38;

Gaps

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156

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STANDARD;

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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision; photoreceptor; Retinal protein; Palmitate; G-protein coupled receptor. Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor. NON_TER
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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2 (POTENTIAL).
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CYTOPLASMIC (PO
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CYTOPLASMIC (POTENTIAL).
BY SINILARITY.
RETINAL CHROMOPHORE (BY SIMILARITY).
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CYTOPLASMIC (
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EXTRACELLULAR (POTENTIAL)
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Matches 51;
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SEQUENCE
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DOMAIN 1
TRANSMEM 37
DOMAIN 62
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DOMAIN 99
TRANSMEM 114
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PROSITE; PS00238; OPSIN; 1.
PRAM; PF00001; 7tm_1; 1.
Photoreceptor; Retinal protein; Transmem
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                                                                                                           CIPID
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+
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Meopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Perciformes; Gobioidei; Gobiidae; Pomatoschistus.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES
VISION IN DIM LIGHT.
PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
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MISCELLANEOUS: THIS RHODOPSIN HAS AN ABSORPTION MAXIMA AT 501 I
MISCELLANEOUS: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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                               Similarity 19.9
51; Conservative
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39409 MW;
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                                         5.0%;
                                 31;
                              Score 79; DB 1
Pred. No. 2.1;
31; Mismatches
                                                                       RETINAL CHROMOPHORE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
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BY SIMILARITY.
BB8CE379AFED4656 CRC64;
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EXTRACELLULAR.
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CYTOPLASMIC.
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5 (POTENTIAL).
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-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES VISION IN DIM LIGHT.
-1- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
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15-JUL-1998
15-JUL-1999
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Neopterygii; Teleost
Zeiformes; Zeidae; Z
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O42604;
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Zeus faber (John Dory).
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BE PHOSPHORYLATED.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED OPSIN SUBFAMILY.
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(Rel.
(Rel.
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Euteleostei; Acanthopterygii; Percomorpha;
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DOMAIN This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). PRINTS; PRO0237; GPCRRHODOR PRINTS; PR00238; OPSIN. PRINTS; PR00579; RHODOPSIN. PFAM; PF00001; PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; PROSITE; PS00238; OPSIN; 1. Phosphorylation; Photoreceptor; GCRDB; GCR\_2445; EMBL; Y14484; 1 37 62 74 99 114 CAA74832.1; -. Retinal protein; Transmembrane; Glycoprotein;
n; Lipoprotein; Palmitate; G-protein coupled r

EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL). ; Lipoprotein; 36 E 36 C 73 C 113 E 113 E 152 C 7tm\_1; 1. GPCRRHODOPSN EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL). CYTOPLASMIC CYTOPLASMIC 2 (POTENTIAL (POTENTIAL) μ (POTENTIAL). (POTENTIAL) receptor a collaboration. MBL outstation -1

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Query Match 5.0%; Score 79; DB 1; Length 354; **Best Local Similarity 18.7%; Pred. No. 2.1; **Matches 53; Conservative 35; Mismatches 87; Indels 108; Gaps
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                                                                                                   Db ~ 202 SFVIYMFVCHFSIPLTIIF----FCYGRLLCAVKDAAAAQQESETTQRAEREVSRMVVIM 257
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314 RHCM----ITTLCCGKNP------FEEEEGASTTASKTE 342
                       226 -YCADLSEIRVRCCARRTRRLMLRAVRIIAEETTAMLYSCRTE 267
                                                 258 VIGFLICWLPYASVAWFIFTHOGSEFGPVFMTIPA----FFAKSSAIYNPMIYICMNKQF 313
                                                                          188 ---YLRLWYD-------GHYGSYVPAMSFGYSALHCGILNNIYVLCCS--- 226
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2 BY SIMILARITY.
15 BY SIMILARITY.
187 BY SIMILARITY (BY SIMILARITY).
296 PALMITATE (BY SIMILARITY).
322 PALMITATE (BY SIMILARITY).
39662 MW; A97D383F88E86DB3 CRC64;
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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044515 caenorhabdi
067148 aquifex aeo
097180 drosophila
023017 arabidopsis
09w6a8 brachydanio
023666 arabidopsis
024416 fragaria an
021884 caenorhabdi
097285 plasmodium
       Q9yh02 sparus aura
Q22130 caenorhabdi
O18735 canis famil
Q9yh05 diplodus an
Q9yh03 sarpa salpa
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071106; PRELIMINARY; PRT; 219 AA.
071106; Created)
01-AUG-1998 (TIEMBLIEL 07, Last sequence update)
01-AUG-1998 (TIEMBLIEL 08, Last annotation update)
01-NOV-1998 (TIEMBLIEL 08, Last annotation update)
ADENOVIRUS 3 COMPLETE GENOME.
Boyine adenovirus type 3 (Mastadenovirus bos3).
PAIRUSES; dsDNA viruses, no RNA stage; Adenoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-WBR-1;
BAXI M.K., REDDY P.S., Z:
BABIUK L.A., TIKOO S.K.;
Virus Genes 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-WBR-1;
LEE J.B., BAXI M.K., IDAMAKANTI N.,
PYNE C., BABIUK L.A., TIKOO S.K.;
Virus Genes 0:0-0(1998).
                                                                                                                                      STRAIN-WBR-1;
REDDY P.S., IDAMAKANTI N., ZAKHARTCHOUK A.N., BAXI M.K.,
PYNE C., BABIUK L.A., TIKOO S.K.;
PYNE C., BABIUK D.A., TIKOO S.K.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF030154; AAD09737.1; -.
SEQUENCE 219 AA; 26028 MW; 092D5CCD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                   REDDY P.S., IDAMAKANTI N., ZAKHARTCHOUK A.N PYNE C., BABJUK L.A., TIKOO S.K.; "Nucleotide sequence, genome organization, bowine adenovirus type 3."; J. Virol. 72:1394-1402(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-WBR-1;
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           Score
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           223.5; DB 12;
No. 7.7e-16;
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MEDLINE; 95351046.
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"Sequence analysis of p
adenovirus type 3.";
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Q84211;
Q84211;
Q1-NOV-1996 (TrEMBLrel. 0)
Q1-NOV-1996 (TrEMBLrel. 0)
Q1-NOV-1996 (TrEMBLrel. 0)
Q1-NOV-1996 (TrEMBLrel. 0)
MASTADENOVIRUS 19.8 KDA porcine adenovirus 3.
                                                                                                             SEQUENCE FROM N.A.
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                                                                     Viruses; dsDNA viruses,
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Submitted (JAN-1996) to the
EMBL; L43363; CAB24462.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 --GHVGSVVDAMSFGYSALHC-GILNNIVVLCCSYCADLSEIRVRCCARRTRRLMLRAVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSLQCRSAAVYFQGLVKQCVHGAQFDRVYWYFRRELSKLSSVFLAYVGSVYVNNVHLIYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSTFMIEEGSYIRCTPWGECLWVKGNSCIYLILICRSCNPLTEMSVNCCLKRCKQKIRYM 176
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45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 AA;
                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                              DERBYSHIRE J.B.;
f putative pVIII,
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1 POLYPEPTIDE (ORF 8).
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;he EMBL/GenBank/DDBJ databases.
                                                                                                                                                 RNA stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 180; DB 12;
Pred. No. 2.1e-11;
                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                               Adenoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 163;
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                                                                                                                                             Mastadenovirus.
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                              O.f.
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                            porcine
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Best Local S
Matches 45
                                              O71108 PRELIMINAKI,
O71108;
O71108;
O71108;
O71081998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ADENOVIRUS 3 COMPLETE GENOME.
Bovine adenovirus type 3 (Mastadenovirus bos3).
The constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constan
                  SEQUENCE FROM N.A. STRAIN-WBR-1;
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Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF083132; AAC99443.1; -. SEQUENCE 163 AA; 19786 MW; DAE89AID CRC32;
                                                                                                                                                                                                                                                                                                         111 AIGAQRRG-----RKQQF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-6618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REDDY P.S., IDAMAKANTI N., SONG J.Y., I CHA S.H., BAE Y.T., TIKOO S.K., BABIUK "Nucleotide sequence and transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 LASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFMSSVFMRGRHLIYLRLWYD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REDDY P.S., IDAMAKANTI N., DERB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 95407103.

MEDDY P.S., TUBOLY T., DENNIS J.R., DERBYSHIRE J.B., NAGY E.;

"Comparison of the inverted terminal repetition sequences from five porcine adenovirus serotypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virus Res.
[2]
                                                                                                                                                                                                                                                                                                                                             252 IIAEETTAMLYSCRTERRRQOF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      idenovirus type 3.";
Zirus Res. 0:0-0(1999).
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                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence and transcription denovirus type 3.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            irology
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J.B., BAXI M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   μ
                                                                                                                                                                                                                                                                                                                                                                              RMFHMGEVI-----YCDGDYANYIVLVCRRCHELSEPVARRCAQRLRHWLKLAAE
                                                                                                                                                                                                                                                                                                                                                                                                                --GHVGSVVPAMSFGYSALHC-GILNNIVVLCCSYCADLSEIRVRCCARRTRRLMLRAVR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRSIMREI IRGCEYNRIFWWFREAVNLPSVSRVMYVGSVMFRGAHLMYIKIMYDCDLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity
45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 2.1e-11;
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K L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        map
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porcine adenovirus type
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                                                                  Mastadenovirus
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RESULT OF ACCOUNTS

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IDAMAKANTI N.,

REDDY P.S.,

ZAKHARTCHOUK

A.N.,

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STRAIN-WBR-1;
REDDY P.S., IDAMAKANTI N., ZAKHAMALL.
PYNE C., BABIUK L.A., TIKO S.K.;
SSLUMMITTED (COT-1997) to the EMBL/GenBank/DDBJ
CERBL; AF030154; AAD09739.1;
PROPRIECE 268 AA; 31016 MW; BEAA16AF CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-WBR-1;
BAXI M.K., REDDY P.S., Z.
BABIUK L.A., TIKOO S.K.;
Virus Genes 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYNE C.,
Virus Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REDDY P.S., IDAMAKANTI N., ZAKHARTCHOUK A.N., E PYNE C., BABIUK L.A., TIKOO S.K.; "Nucleotide sequence, genome organization, and bovine adenovirus type 3."; "Yirol. 72:1394-1402(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 98
REDDY P.S.,
                                                                                                                                                                                                                                                                                                                                                                                       P89027 PRELIMINARY; PRT; 220 AA. |
P89027;
D1-MAY-1997 (TrEMBLrel. 03, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update
E4.2 PROTEIN (25.6 KD PROTEIN).
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                                                                                                                                                           MEDILIE: 96240641.

WRATI S., BROOKES D.E., STRIKE P., KHATRI A., BOYLE: "Unique genome arrangement of an ovine adenovirus: 1 "Unique genome arrangement of account adenovirus: 1 new proteins and proteinsae cleavage sites.";
Virology 220:186-199(1996).
                                                                                                                                                                                                                                                                                                                                                                          Ovine adenovirus
  MEDLINE; 97271311.

XU Z.Z., HYATT A., BOYLE D.B., BOY

"Construction of ovine adenovirus

deletion of related terminal regic
                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses,
                                                                                            SEQUENCE FROM N.A.
STRAIN-OAV287;
                                                                                                                                                                                                                                                                                   STRAIN-OAV287
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272
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nes 0:0-0(1998).
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Pred. No. 2e
    region sequences.
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                          BOTH G.W.;
rus recombinants
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2e-09;
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fication of
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Best Local S
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Q9Y748;
Q1-NOV-1999
Q1-NOV-1999
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ
EMBL; U40839; AAD45954.1; .
SEQUENCE 220 AA; 25401 MW; DCAFF782 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 98277079.
KHATRI A., BOTH G.W.;
KHATRI A., BOTH G.W.;
Tidentification of transcripts
adenovirus OAV287.
Virology 245:128-141(1998).
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[3]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGERMAYR K., PARSON W., STOFFLER G., HAAS H.;
"Expression of atrC - encoding a novel member of the cassette transporter family in Aspergillus nidulans cycloheximide.";
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Eurotiales; Trichocomaceae;
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Eukaryota: Fungi: Ascomycota: Euascomycetes:
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EMBL; AF082072; AAD25925.1;
PROSITE; PS00211; ABC_TRANSPORTER; 2.
ATP-binding; Transport.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                              LIVLYRCRQ-CLPCSSGRFQQSHLIFQFPLPAMASEMLHKGNEWGIIYIVLAVSVLICYA 775
GLGFFFTVAASFLSGTYRSRYFAAMLNQDVSFFEEEDQSAGVMTGQLSTDPQRIEDLISL
                                                                                                                                                                                                      LVILRKCMHVCLCCAN------
                                                                 G------GQVLASWFRMVVDGAMFNQRFIWYRE-----VVNYNM---PKEVMFMSSV 179
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50; Conservative
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(TIEMBLrel. 12, Last sequence update)
(TIEMBLrel. 12, Last annotation update)
RIER PROTEIN ATRC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 141984 MW;
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                                                                                                                                                                                                                                                                              Score 90; DB
Pred. No. 0.65
36; Mismatches
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dulans - is
                                                                                                                                                                                                                                                                                                                                                Length 1293
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RECUESTRAIN-BRISTOL N2;

MEDLINE; 94150718 N., ANDERSON K., BAYNES C., BERKS M.,

REAL MEDLINE; 94150718 N., CONNELL M., COPSEY T., COOPER J., COULSON A.,

REAL CRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

REAL CRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

REAL CRANTON M., CREEN P., HAWKINS T., LAITSTER M., JOHNSTON L.,

RAL JONES M., KERSHAW J., KIRSTEN J., LAISTER M., JOHNSTON L.,

RAL LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RAL LIGHTNING J., LLOYD C., RIFKUN M., MORTIMORE B., O'CALLAGHAN M.,

RAL PARSONS J., PERCY C., RIFKUN M., ROOPEA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALLON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,

RT "2.2 MD of contiguous nucleotide sequence from chromosome III of C.

RT "2.2 MD of contiguous nucleotide sequence from chromosome III of C.

RT "2.2 MD of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                             WATERSTON R.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF038619; AAB92076.1; -
SEQUENCE 494 AA; 56780 MW; F59CC020 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATTUNG S., GOELA D., HI
Submitted (DEC-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TIEMBLIEL 06, 01-JUN-1998 (TIEMBLIEL 06, 01-NOV-1998 (TIEMBLIEL 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            888 QERTTRLYLESARFATEAISAIRTVASLTLEEKVIQMYDERLSHTSPKFIRITL 941
                                                            GHVGSVVPAMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCARRTRRIMLRAVRIIA 254
                                                                                                                                                                        NILYLFLLACLDILVELCFMLIFPASLVWDYFRVELLYTCWHFYIKYVS-----TVGQ
                                                                                                                                                                                                                                               EINDTCAEDP---PQADAFRMILIVIIGTVVCSLGI-----VLNTFLLLSLRRLDVFRS 103
                                                                                                    VLIAASTLLIVAASFERYICSLKSSIQFSPQRRFLFISIVGACALFMKGSVFFELEL---
                                                                                                                                      VLASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFMS----SVFMRGRHLIYLRLWYD 194
                                                                                                                                                                                                             CMHVCLCCANIDIMTS---MMIHG-----YESWALHCHCSSPGSLQCIAGGQ 139
                                                                                                                                                                                                                                                                                   ETRATILEDHPLLPECNTLTMHNVSYVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRK 95
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                              -QSLPHCPPFQNLRL-----DLSEI----TRRTKTYLIYGKLIFS
                                                                                                                                                                                                                                                                                                                                          5.5%;
20.2%;
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to the EMBL/GenBank/DDBJ databases.
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Rhabditidae; Peloderinae; Caenorhabditis.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                           Score 87; DB 5; Length 494; Pred. No. 0.45; Indels:
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067148
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Best Local :
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097180;
01-MAY-1999 (TIEMBLIFEL 10, C
01-MAY-1999 (TIEMBLIFEL 10, L
01-MOV-1999 (TIEMBLIFEL 12, L
                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Etarygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
MEDLINE; 99147028.
FELDMANN P., EICHER E.N., LEEVERS S.J., HZ
"Control of growth and differentiation by
                                           STRAIN=OREGON-R;
MEDLINE; 9914702
                                                                                                                                                                                          RASGAP.
                                                                                                                                                                                                         RASGAP PROTEIN.
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LEN GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AE000720; AAC07109.1; -. SPA33D85 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 98196666.

DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;

"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                067148
067148;
01-AUG-1998
01-AUG-1998
01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                    184 IWGMIGGKVSATW-----AKFHHP-KWYREVV 209
                                                                                                                                                                                                                                                                                                                                                                                                                             132
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                                                                                                                                                                                                                                                                                                                                                                                                                        LQCIAGGQVLASWFRMVVDGAMFNQRFIWYREVV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HVCLCCANIDIMTSMMI-----HGYESWALHCH-----
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Last sequence update)
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Pred. No. 0.25
20; Mismatches
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RasGAP, a
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Mol. Cell. Biol. 19:1928-1937(1999).
EMBL; AJ012609; CAAL10073.1; -
HSSP; P20936; IMER.
PROSITE; PS00509; RAS_GTPASE_ACTIV_1; 1.
SEQUENCE 954 AA; 107950 MW; 0DB2B774 CRC32;
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Bukaryota; Viridiplantae; Streophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streophyta; Bubaryophyta; Tracheophyta;

euphyllophytes; Spermetophyta; Magnollophyta; eudicotyledons;

core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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OSBORNE B.I., VYSOTSKAIA V.S., TORIUMI M., YU G., OJI O., LIU
OSBORNE B.I., VYSOTSKAIA V.S., TORIUMI M., YU G., OJI O., LIU
LI J., HOANG L., BUEHLER E., CONWAY A.B., CONWAY A.R., DEWAR F
FING J., KIM C., KURTZ D., LI Y., SHINN P., SUN H., DAVIS R.W.
ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-1997) to the EMBL/GenBank/DDBJ EMBL; AC002376; AABB0622.1; -
MENDEL; 25798; Arath;1088;25798.
PFAM; PF00544; pec_lyase; 1.
                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-CV. COLUMBI
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"Cloning and characterization of six zebrafish photoreceptor cDNAs and immunolocalization of their corresponding proteins. Vis. Neurosci. 0:0-0(1999).
EMBL; AF109372; AAD24755.1; --
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
SEQUENCE 354 AA; 39483 MW; 535F4C88 CRC32;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Ostariophysl; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDNPVNPRPGTL-RHAVIQDRPL------WIVFKRDMVIQLKQELIVNSFKTIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDHPLLPECNTLTMHNVSYVRGLPCSVGFTLIQEWVV-PWDMVLTREELVILRKC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YMRDKAMOVTIAYNHFGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAISIFGSSHYW----IDHNSLSHCADGLVDAVMGSTAITISNNHLTHHNEVMLLGHSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGANVHIANGGCITIQFVTNVIVHG-----LHIHDCKPTGNAMVRSSETHFGW-RTMADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---MHYCL-CCANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGQYLASWFRMVVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VV--PAMSFGYSALHCGI 215
                                                                                                                                                                                                                     FSTIVFCYGQLLITLKLAAKAQADSASTQKAEREVTKMVVVMVFGF
                                                                                                                                                                                                                                                                                                                                                                   HCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFM------
                                                                                                                                                                                                                                                                                                                                                                                                                       CKIEGFISTIGGMVSLWSLA-----VVALERWLVICKPLGNFTFKTPHAIAG----
                                                                                                                                                                                                                                                                      --SSVFMRGRHLIYLRL---
                                                                                                                                                                                                                                                                                                                     -CILPWCMALAAGLPPLLGWSRYIPEGLQCSCGPDWYTTNNKFNNESYVMFLFCFCFAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 21.7
43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR00807; AM
CE 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 5.2%;
1 Similarity 24.1%;
40; Conservative 1
(TrEMBLiel.
(TrEMBLiel.
(TrEMBLiel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                    PRELIMINARY
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A; 47770 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.3%;
  12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 83; DB
Pred. No. 0.81
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 84.5;
Pred. No. 0.
Created)
Last sequence up
                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                         -WYDGHVGSVVPAMSFGY 208
                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
0.81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RI lyase from
RL Plant Mol.
DR EMBL; U635
DR MENDEL; 26
EMBL; W635
CR Lyase
SQ SEQUENCE
Ouery Match
Matches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 35
                                                                                                                              Lyase .
SEQUENCE
                                                                                                                                                         strawberry ripening-specific CDNA with se lyase from higher plants.";
Plant Mol. Biol. 34.867-877(1997).
EMBL; U63550; AAB71208.1;
MENDEL; 26059; Frax;1088;26059.
DFAM; PF00544; pec_lyase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998
01-JAN-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                 Fragaria ananassa (Strawberry).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Fragaria.
                                                                                                                                                                                                                                                                                   MEDLINE; 97435972.
MEDINA-ESCOBAR N., CARDENAS J.,
MUNOZ-BLANCO J.;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 024416;
                                                                                                                                                                                                                                                                 Cloning, molecular characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PECTATE LYASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RULIKAUSKAS R., MCCORMICK S.;
"Identification of the tobacco and Arabidopsis homologues of the pollen-expressed LAT59 gene of tomato.";
Plant Mol. Biol. 34:809-814(1997).
EMBL; U83620; AAB69760.1;
MENDEL; 25560; Arath;1088;25560.
PFAM; PF00544; pec_lyase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyliophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core_eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 97422403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 EDHPLLPECNTLTMHNVSYVRGLPCSVGFTLIQEWVV-PWDMVLTREELVILRKC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAISIFGSSHVW----IDHNSLSHCADGLVERSMGSTAITISNNHLTH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---AMFNQRFIWYREVVNYN------MPKEVMFMSSVFMRGRHLIY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGANVHIANGGCITIQFVTNVIVHG-----LHIHDCKPGNAM-VRSSETHFGW-RTMADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----MHVCL-CCANIDIMISMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDNPVNPRPGTL-RHAVIQDRPL------WIIFKRDMVIQLKQELIVNSFKTIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                               405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 05, (TrEMBLrel. 05, (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
181 AA;
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20088 I
                                                                                                                            45744 MW;
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Last sequence update)
Last annotation update)
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Pred. No. 0.43;
                                                                                                                        2B9944A0 CRC32;
                                                                                                                                                                                                                                                                                                MOYANO E., CABALLERO J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EF3426C6 CRC32;
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                                                                                                                                                                                                                                             sequence homology to
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                                                                   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSENT J., COOPER
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDINER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTMING J., LLOYD C., KCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN J.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VANGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q21884
Q21884;
Q1-NOV-1996
 EMBL; Z77134; CAB00874.1; -. HSSP; P00750; ITPG. SEQUENCE 1603 AA; 175349
                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rha
                                             Nature 368:32-38(1994).
                                                                elegans.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 94150718
                                                                                                                                                                                                                                                                                       Submitted (JUL-1996)
                                                                                                                                                                                                                                                                                                         BASHAM V
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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175349 MW;
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                                                                                                                                                                                                                                                                                    the EMBL/GenBank/DDBJ databases
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12,
                                                                                                                                                                                                                                                                                                                                             pda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
 38FFA309 CRC32;
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                                                                                                                                                                                                        COULSON A.,
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Best Local S
Matches 44
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YREVVNYNMPKEVMFMSSVFM 181
                                                                                      TSGCKYEYIMNQEYTCQSAGDTFTMETTITTNEVTIMRTQRAYCSDLIGCINGGIMLGGN 1088
                                                                                                                                        GFSPDPSFDRFSRDLTYATHQQPVIHL---SSTLQSDPSIDVTSYDNNNNIAFTSLFTKR 1028
                                     CQCVNGYTS--LHCEVPTCQNGGSVVDFKCQCPSIYDG--
                                                          SMMIHGYESWALHCH----CSSPGSL-----QC--IAGGQVLASWFRMVVDGAMFNQRFIW
                                                                                                               GLPCSVGFTLIQEW-----VVPWDMVLTREELVILRKCMHVC---LCCANIDIM---T
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                               5.1%;
21.9%;
                                                                                                                                                                                                  29;
                                                                                                                                                                                                Score 82; DB Pred. No. 5.7; Mismatches
                                                                                                                                                                                                           DB
5.7;
                                                                                                                                                                                                                         <u>ن</u>
                                                                                                                                                                                                 82;
                                                                                                                                                                                                                         Length 1603;
                                     -DSCQYTTCNTW
                                                                                                                                                                                                46;
                                                                                                                                                                                             Gaps
                                                             160
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Called Control

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1 Similarity 24.447; Conservative

5.2%;

25;

Score 82.5; D Pred. No. 1.1; 25; Mismatches

DB 10; 66;

Length Indels

55;

Gaps

12;

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1136 --NEVETHDPREYNEQQIVEV 1154

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SERVER
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                                                                                                                                                                     220 OPIVEELMKFLPKEKOILMYSATFPVTVKEFRAIYLS---DAHEINLMDELTLKGITQYY 276
                                                                                                                                                                                                                                                                                                                                                             117 PLLERCNT----HKNFIQGL------ILVPTRELALQTSAMIKELGKHMKVQCMV 161
                                                                                                                               255 210 A-----LHC------GILNNIVVLCCSYCADLSEIRVRCCARRIRRLMLRAVRIIAE
                                                                                                                                                                                                                                                                      162.TTGGTSLREDIMRLYN--VVHILCGTPGRILDLANKDVANLSGCHIMVMDEADKLLSPEF 219
                                                                                                                                                                                                                  106 IDIMTSM---MIHGYESWALHCHCSSPGSLQCIAGGQV--LASWFRMVVDGA--MFNQRF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-3D7;

OLIVER K., BOWMAN S., HARRIS D., LAWSON D., QUAIL M., BARRELL B.;

Submitted (FEB-1999) to the EMBL/GenBank/DDBU databases.

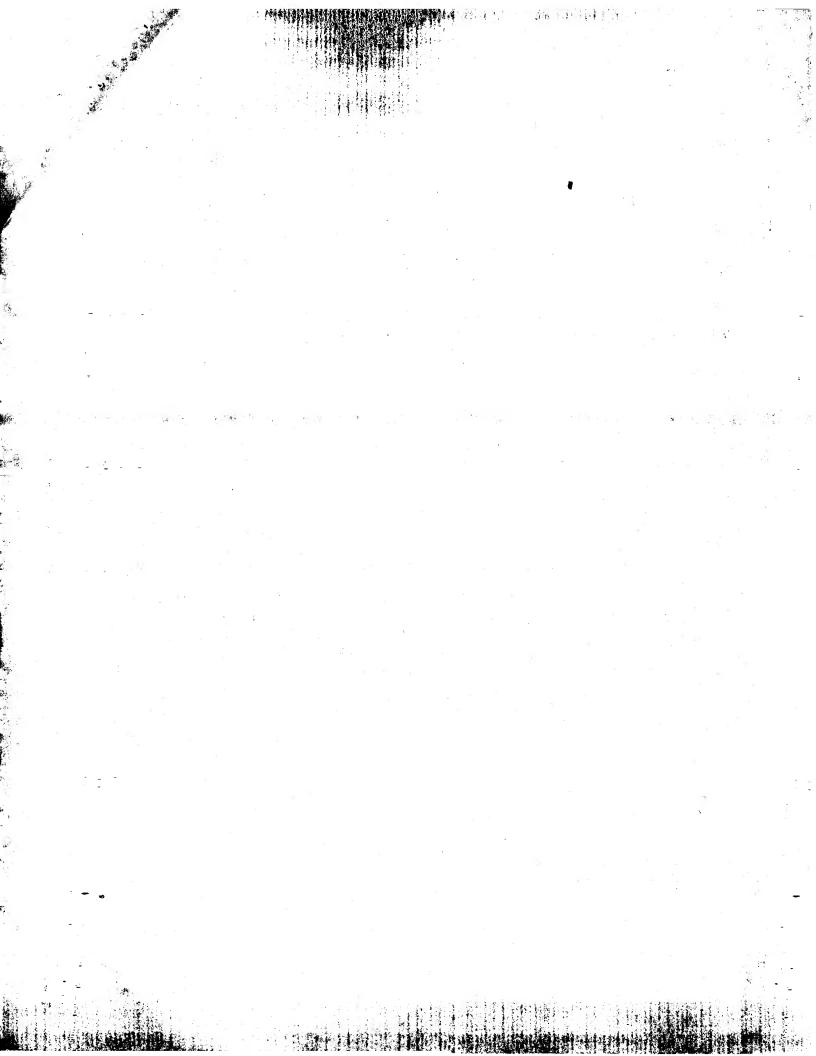
EMBL; AL034559; CAB39031.1; -.

PROSITE; PS00039; DEAD_ATP_HELICASE; 1.

ATP-binding; RNA-binding; Helicase.

SEQUENCE 433 AA; 49413 MW; C419B9EF CRC32;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MOV-1999 (TrEMBLrel. 12, Last annotation update)
pFC0915W PROTEIN.
                       316 KITELGYS-----SFYIHARMSQTHRNRVFHDF 343
                                                                                         277 AFVKERQKVHCLNTLFAKLQINQAIIFCNS-----
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karyota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Search completed: June 23, 2000, 10:07:44 Job time: 947 sec



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Run on:
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Maximum DB seg length: 1000000
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2: pir2:
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4: pir4:
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Gapop 10.0 , Gapext 0.5
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621
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13.0
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          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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P65 protein - Ectr
Platelet-activatin
myelin/oligodendro
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myelin/oligodendro
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ALIGNMENTS	QQBEWI QQBEWI C70627 S52046 S52046 S09829 PH1661 PL0100 G70903 ASLJSW T15845 S60183 T02691	QMXRWT
	DIS2 protein - hum DNA-directed RNA p hypothetical prote deoxyribodipyrimid hypothetical prote If heavy chain vr If heavy chain pre hypothetical prote vif protein - huma hypothetical prote protein ExsB - Rhi glossyl protein gl	capsomere protein

## Q4ADD2 early E4 13K protein - human adenovirus 2 C;Species: Mastadenovirus h2 (human adenovirus 2) A;Note: host Homo sapiens (man) C;Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 04-Mar-1994 A;Map position: 95.0-96.0 C;Superfamily: adenovirus early E4 13K protein C;Keywords: early protein R;Herisse, J.; Rigolet, M.; Dupont de Dinechin, S.; Galibert, F. Nucleic Acids Res. 9, 4023-4042, 1981 A;Title: Nucleotide sequence of adenovirus 2 DNA fragment encoding A;Reference number: A93733; MUID:82059444 A;Accession: A03806 RESULT 밁 Š A;Molecule type: DNA A;Residues: 1-114 (HER> A;Note: this probable protein was assigned by correlating EM data and S1 digestion st C; Accession: A03806 Genetics: Query Match 99.5%; Best Local Similarity 99.1%; Matches 113; Conservative Score 618; DB 1; Pred. No. 7.1e-60; Mismatches Length 114; Indels 0 for the Gaps 60 carboxylic

	submitted to the EMBL Data Library, June 1993 A; Reference number: S33928
:	A; Note: the authors translated the codon low for residue of as 1): R; Sprengel, J.
	A;Cross-references: EMBL:X51800
	A; Residues: 1-120 < HOG>
	A; MOLECULE type: DNA
	A;Accession: S10865
	A; Reference number: S10860; MUID: 90272430
ncoding the	A; Title: Nucleotide sequence of the right 10% of adenovirus type 12 DNA encoding the
	Nucleic Acids Res. 18, 3065-3066, 1990
	R; Hogenkamp, T.; Esche, H.
	C; Accession: S10865; S33953
,	C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-Aug-1999
	C; Species: Mastadenovirus h12 (human adenovirus 12)
٠.	early E4 13K protein - human adenovirus 12
:	\$10865
	RESULT 2
: .	
	Db 61 NYTTERAKERDRERESVCHARTWECFEKYDYVERSIWHDTTTNTISVVSAHSVO 114
	OV 61 NYYTERSKRRDRRRRSVCHARTWFCFRKYDYVRRSIWHDTTTNTISVVSAHSVQ 114

A; Accession: S33953

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RESULT 3
                                                                                                                         A; Reference number: S29651; MUID:93160241
A; Accession: S29651
                                                                                                                                                                    R;Pearson, J.A.; Tyler, M.I.; Retson, K.V.; Howden, M.E.H. Biochim. Biophys. Acta 1161, 223-229, 1993
A;Title: Studies on the subunit structure of textilotoxin, a ces of all the subunits.
                                                                                                                                                                                                                                                                          textilotoxin chain A - eastern brown snake
C:Species: Pseudonaja textilis (eastern brown snake)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #
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A; Molecule type: DNA
A; Residues: 1-373 <WHI>
A; Cross-references: GB: AEO01952; GB: AEO00513; NID: 96458725; PIDN: AAF10581.1; PID: 96458725
A; Cross-references: GB: AEO01952; GB: AEO00513; NID: 96458725; PIDN: AAF10581.1; PID: 96458725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTP triphosphohydrolase-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03:Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession:.F75449
R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
K;White, 0.; Eisen, J.A.; Heidelberg, J.F.; McDonald, L.; Utterback, T.; Zalevski, C.; McShen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalevski, C.; McSishi, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250
A;Accession: F75449
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A;Residues: 1-120 <SPR>
A;Cross-references: EMBL:X73487; NID:g313361; PIDN:CAA51902.1; PID:g313387
C;Superfamily: adenovirus early E4 13K protein
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                                                         Residues: 1-118 <PEA>
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                                      Superfamily:
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Matches 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 YYNYYTER 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 QNECVGWL-----GVAYSAVV--DVIRAAAHEGVYIEPEARGRL----DALREWI 58
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                              phospholipase
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40.2%; Pred. No. 8.4e-20;
ative 23; Mismatches 41
                                   A2
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7; Mismatches
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                A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095 C:Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: heterotetramer; immunoglobulin
                                                                                        A; Molecule type: mRNA
A; Residues: 1-155 < CHA>
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-129/Domain: immunoglobulin homology <IMM>
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C;Accession: S31511
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M. submitted to the EMBL Data Library, December 1992
                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
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A; Status: preliminary
                                           A; Accession: S31511
                                                                       A;Description: Dominance of clonotypic patterns and variable A;Reference number: S31509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Start codon: TTG
C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cobalamin biosynthesis protein N homolog - Methanococcus jannaschii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 YDYVRRSIWHDTTTN----TISVVSAH 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 -VDVIRAAAHEGVYIEPEARGRLDALREWIYYNYTERSKRRDRRRRSVCHARTWECERK 88,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NYYTERS----KRRDRRRRSVCHARTWF--CFRKYDYVRR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 CDSQNECVGWLGVAY------SAVVDVIRAA-AHEGVYIEPEARGRLDALREWIYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 CANKYKRPGWHYANYGCYCGSGGRGTPVDDVDRCCQAHDKCYEDAE---KLGCYPKWTTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYEEPRPMPWQGIYYKGKYFETLDD-----YLNYLKELGRDLDKPIIGVLFYRNWFVANN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYYCGANGPYCKTRTKCQRFVCNCDVVAADCFASYPYNRR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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23.8%;
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29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 72.5; DB
Pred. No. 8.5;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80; DB 2; Length 118; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 1232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
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                                                                                                       gene usage of anti-DNA-a
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submitted to the EMBL Data Library, August 1992
A; Reference number: $24675
A; Accession: $24675
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Cross-references: EMBL:214256; NID:g59257; PIDN:CAA78622.1; PID:g59258
A; Cross-references: EMBL:214256; NID:g59257; PIDN:CAA78622.1; PID:g59258
C; Superfamily: POZ domain homology
                                                                                                                                                                                                                                                                                                                     C;Accession: JC5021; PC4207
R;Rarasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yokoyama
R;Rarasawa, K.; Ruge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yokoyama
LJ: Biochem. 120, 838-844, 1996
A;Title: Cloning, expression and characterization of plasma platelet-activating factor-
A;Reference number: JC5021; MUID:97103479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: For F; 12-115/Domain:
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                                                               A; Experimental source: liver
C; Comment: This enzyme converts platelet-activating factor to an inactive metabolite ly
C; Keywords: glycoprotein; hydrolase
C; Keywords: glycoprotein; hydrolase
                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-436 <KAR1>
A;Cross-references: DDBJ:D67037; NID:g1644228; PIDN:BAA11054.1; PID:d1011714; PID:g16442
                                                                                                                                                                                                                                                                                                  A; Accession: JC5021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N; Alternate names: PAF-acetylhydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 platelet-activating factor-acetylhydrolase (EC 3.1.-.-) precursor -
                                                                                                                                                 A; Molecule type: protein
A; Residues: 123-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392
                                                                                                                                                                                                 A; Accession: PC4207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: S24675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Ectromelia virus
Date: 20-Feb-1995 #sequence_revision
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Best Local :
11-21/Domain: signal sequence *status predicted <SIG>
;22-436/Product: platelet-activating factor-acetylhydrolase *status predicted
;76;200,324/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Species: Cavia porcellus (guinea pig)
;Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 MYMRNIPTLITTDAFKNAV-----FEILLDII--STNDGEYVYREGY-KVTILLKWLDY 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 VYHDTNYN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 FCFRK-----YDYVRRSIWHDTTTNTIS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 QPPGKG-----LEWIGYIYYTGSATYNPPLKSRVTISVDTSKNQFSLKVSSVTAADTAVY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 EPEARGRIDALREWIYYNYYT-------ERSKRR-DRRRRSVCHART--W 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IWHDTTTN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYITEEQLLCILSCIDIQNLDKKSRLLLYSNTTINMYSSCVKFLLDNKQNRNIIPRQLCL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYYTERS-----KRRDRRRRSVCHARTWF-----CFR-----KYDYVRRS--- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Conservative
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28.1%;
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Pred. No.
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Pred. No. 3
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cell surface antigen 4F2 heavy chain - Rattus leucopus N;Alternate names: neutral amino acid transporter system L-linked protein C;Species: Rattus leucopus C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 23-Jul-1999 C;Accession: S64702; S57719 R;Broeer, S; Broeer, A; Hamprecht, B. Blochem, J. 312, 863-870, 1995
                                                                                                              Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A; Reference number: A70500; MUID:98295987
A; Accession: B70834
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C; Keywords: surface
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                                                                                                                                                                                                                                                                                                                                              hypothetical protein Rv0383c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-527 <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S64702; MUID: 96128073
A; Accession: S64702
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A; Title: The 4F2hc surface antigen is necessary
                                                                                                                                                                                                                                                                                             C; Accession: B70834
R; Cole, S.T.; Brosci
A;Cross-references: GB:AL021931; GB:AL123456; NID:g3261526; A;Experimental source: strain H37Rv
                                                A; Molecule type: DNA
A; Residues: 1-284 <COL>
                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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Best Local S
Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 LGVAYSAVVDVIRAAAHE-----GVYIEPEARGRLDALREWIYY---NYYTERSKRRDRR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 RRSVC-HARTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 Y 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 LGWLGMLAGAVVIIVRAPRCRELPVQRWWHKGALYRIGDLQAFVGPEARG-IAGLKNHLE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 VGWLGVAYSAVVDVIRAAA------HEG-----VYIEPEARGRLDALREWIX 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                      Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
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Pred. No. 17;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4F2 heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                              PIDN:CAA17389.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
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                                                                                                                                                                            the complete
                                 PID:e125
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**60 YNYYTERSKRRDRR** 

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A; Molecule type: DNA
-A; Residues: 1-1083 <ROU>
-A; Cross-references: EMBL: AC003974; NID: g2914688; PID: g2914695
-A; Experimental source: cultivar Columbia
                                             8
                                                                                                                                                                                           A) Map position: 2
A) Introns: 416/2; 1004/2
             ğ
                                                                                                                                                                           A; Note: F24L7.8
                                                                                                       Pest Local :
                                                                                                                                                                                                                                                                                                                                      R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, submitted to the EMBL Data Library, February 1998 A;Description: Arabidopsis thaliana chromosome II A;Reference number: Z14204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ubiquitin-specific proteinase homolog F24L7.8 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Species: Arabidopsis thaliana (mouse-ear cress) # 12-Feb-1999 # text_change 30-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                         A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50557.1; PID:e15164
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-891 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number:
A; Accession: G75014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
G75014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: Pyrococcus
A; Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;anonymous,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         valyl-tRNA synthetase (vals) PAB1255 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
                                                                                                                                                                                                                                 Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary
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Best Local Similarity
             931
                                      14 SQNECVGWLGVAYSAVVDVIRAAHEGVYI------EPEARGRLDALREWIY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           485 EHNFPTA-----LRPGGTDIIRTWAFYTIFRTFKLTGKKPWKDIVIN 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 PPVEKCPVCGAEIEPVTDVLDCWVD---SSITPLIITRWHEAIKGDEEA------KKWF 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 YYNYYTERSKRRDRRRRSVCHARTW---FCFRKYDYVRRSIWHDTTTN 103
                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 YTERSKRRDRRRRSVCHARTWFCFRKYDYVRRSI-----WHDTTINTISVVSAHSV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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     SDNECENWEDLAVDSEEVIVKRDARKKVLINKAPPVLTIHLKRFSQDARGRVSKLSGHVD 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVDIDRRRGRSRR----RKSWARSHGFDYERESTEILKRWTRGVMSTVGDVAAHNV
                                                                                  . Similarity
18; Conserv
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                                                                                                 10.3%;
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23.1%;
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                                                                                             Score 64;
Pred. No.
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Pred. No. 15;
9; Mismatches
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                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                  2.
                                                                                                                                                                                                                                                                                                                                                                                                             M.L.; Brandon, R.C.; Sykes,
                                                                                                                                                                                                                                                                                                                                                                   BAC F24L7 genomic sequence
                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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                                                                            Indels
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                                                                                                              Matches
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65

ERSKRRDRRRRSVCHARTWFCF-----RKYDYVRRSIWHDTTTNTISVV

108

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53

13

26;

Conservative

17;

Mismatches

48;

21;

Gaps

DSQNECV----GW----LGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIYYNYYT 64

DGHIVCVCSIAGWSGETMGLSYCTSKFAVRGAM-ESLQMELRDRG-LEGIKTTTLYPYFA

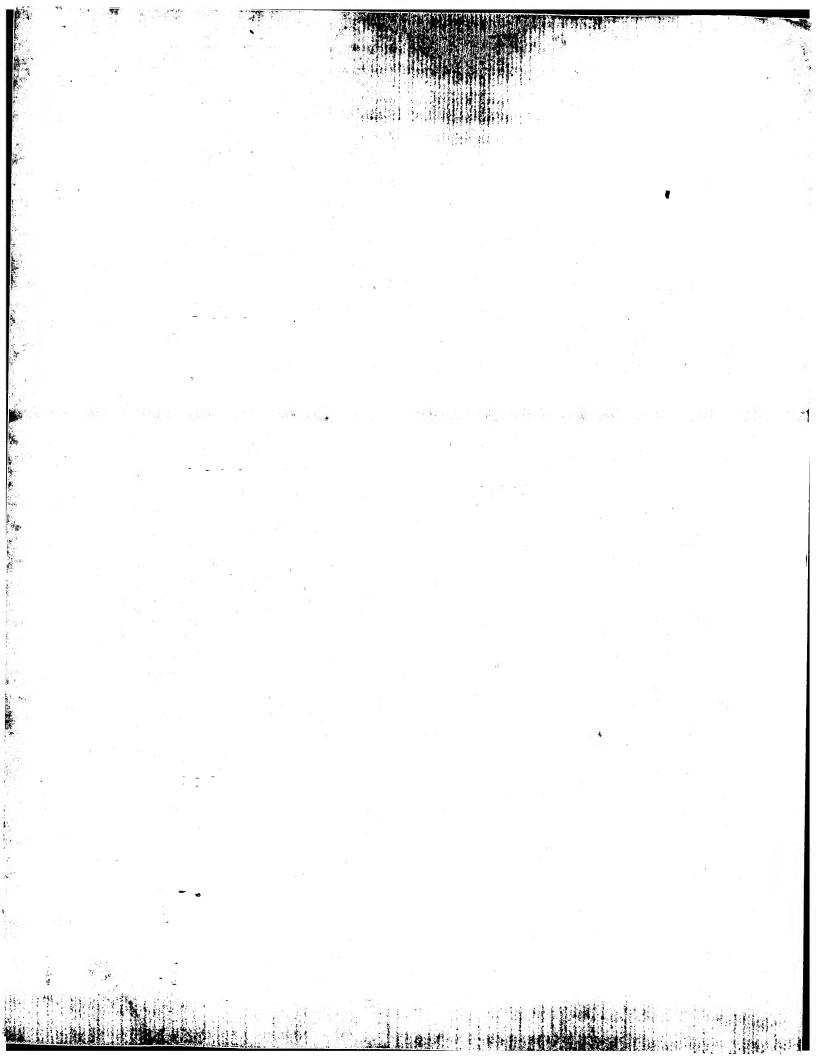
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-264 <BENA
A;Cross-references: EMBL:U49829; NID:g1203924; PID:
                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16188
                                                                                                A; Gene: CESP:F27D9.6
A; Introns: 28/2; 57/3;
                                                                                                                                                                                                                                                                 A; Reference number: Z18473
A; Accession: T16188
                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, February 1996 A; Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                  R; Bentley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A55921
R;Okada, Y.; Yamazaki, H.; Sekine-Aizawa, Y.; Hirokawa, N.
Cell 81, 769-780, 1995
A;Title: The neuron-specific kinesin superfamily protein KIFyA is a unique monomeric...
A;Reference number: A56921; MUID:95292344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-1695 <RES>
A;Cross-references: GB:D29951; NID:g976234; PIDN:BAA06221.1; PID:g976235
C;Superfamily: kinesin-related protein unc-104; kinesin motor domain hom C;Keywords: P-loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1695 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;6-360/Domain: kinesin motor domain nomeroyy samur
F;97-104/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F27D9.6 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinesin family
  Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 PAPPY--CDSQNECYGWLGY-----AYSAVVDVIRAAAHEGYYIEPEAR----GRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALREWIYYNYYTERSKRRDRRRRSV-----CHARTWFCFRKYDY-----VRRSIWHDT- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAEPVDWAFAQRELLEKQGIDMKQEMEQRLQELEDQYRREREEATYLLEQQRLDYESKLE 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALQKQMDSRYYPEVNEEEEEPEDEVQWTERECELALW-AFRKWKWYQFTSLRDLLWGNAI 731
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                                                                                           117/2; 173/3; 231/2
10.2%;
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Pred. No. 97;
19; Mismatches
  Score 63.5;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                              cosmid F27D9
                        ₽B
                                                                                                                                                                 PID:g1203928; PIDN:AAA93385.1; CESP:F2
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                   Length 264;
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64 RTPMILENNMRPTC---TWFPFMSIRSCSKRMVDSILKEKVHAFVPSYITLI 112

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Page 5
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"Db - 354 WIGKPRSIVEGVCYRYDPSNDTIDSIKAVPKENILATFKGN-----WRNCIFYSYAGESE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
Search completed: June 23, 2000, 10:05:47 Job time: 1752 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        robable involvement in ergosterol biosynthesis - fission yeast (Schizosaccharomyces pom
|Species: Schizosaccharomyces pombe
|Pate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
|Accession: T40584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: DNA Residues: 1-516 <SEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:AL035216; PIDN:CAA22812.1; GSPDB:GN00067; SPDB:SPBC646.08c Experimental source: strain 972h-; cosmid c646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. bmitted to the EMBL Data Library, January 1999 Reference number: Z21938 Accession: T40584
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Copyright (c) 1993 - 2000 Compugen Ltd
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E413_ADE02
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Tyler M.I., Barnett D., Nicholson P.,
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Pearson J.A., Tyler M.I., Retson K.V., Howden M.E.H.;

"Studies on the subunit structure of textilotoxin, a potent
"presynaptic neurotoxin from the venom of the Australian common bro
snake (Pseudonaja textilis). 3. The complete amino-acid sequences
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae;
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"Nucleotide sequence of the right 10% of encoding the entire region E4.";
Nucleic Acids Res. 18:3065-3066(1990).
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Matches 29
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RI Biochim. Biophys. Acta 915:210-216(1987).

C -!- FUNCTION: POTENT PRESYNAPTIC NEUROTOXIN POSSESSING PHOSPHOLIPASE

C ACTIVITY. SUBUNIT A IS LETHAL TO MICE AT 4 MG/KG (I.V.). IT IS

C ESSENTIAL FOR THE NEUROTOXICITY OF TEXTILLOTOXIN. SUBUNIT A

POSSESSES A LOW PHOSPHOTIPASE ACTIVITY.

C -!- FUNCTION: PAZ CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE

C -!- FUNCTION: PAZ CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE

C -!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-

C -!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-

C -!- GATALYTIC ACTIVITY: ACTU ANION.

C -!- SUBUNIT: PENTAMER OF THREE NON-COVALENTLY LINKED SUBUNITS A, B,

C -!- MISCELLANDOUS: ALL SUBUNITS ARE NECESSARY FOR MAXIMM LETHALITY.

C -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE AZ FAMMILY.

B PIR. $296571 . $20651
                                                                                                                                                                                                                                            RP54_RHIME STANDARD; PF
P17263; Q59751;
01-AUG-1990 (Rel. 15, Created)
15-FEB-2000 (Rel. 39, Last seque
15-FEB-2000 (Rel. 39, Last annot
RNA_POLYMERASE SIGMA-54 FACTOR (
                                                                                 MEDIINE; 87222100.

MEDIINE; 87222100.

Ronson C.W., Nixon B.T., Albright Philodoline mellioti ntrA (rpoN) gene "Arabolic functions.";

"Anatabolic functions.";
MEDIINE; 89197760.

Albright L.M., Ronson C.W., Nixon B.T., Ausubel F.M.;

"Identification of a gene linked to Rhizobium meliloti ntrA whose product is homologous to a family to ATP-binding proteins.";
                                                                                                                                                                                                                                                                                                                                  RHIME
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                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                    Rhizobium meliloti.
Bacteria; Proteobacteria;
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                                                                                                                                                                                           Rhizobiaceae;
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PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
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HSSP; P00609; 2NOT.
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2; Mismatches
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(VERSION 1).
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                                                                                                                                                                                           P42546;
01-NOV-1995 (Rel. 32, Las
01-NOV-1995 (Rel. 32, Las
01-NOV-1995 (Rel. 32, Las
HYPOTHETICAL 25.6 KD PROT
Bacteriophage L2
Viruses; dSDNA viruses, n
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EMBL; M24926; AAA26349.1; -.
PRINTS; PRO0045; EMBAA54FCT.
PROSITE; PS00717; SIGMA54_1; 1.
PROSITE; PS00718; SIGMA54_2; 1.
--PROSITE; PS50044; SIGMA54_3; 1.
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             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 94215869.
Maniloff J. Kampo G.J., Dascher C.C.;
"Sequence analysis of a unique temperature phage: mycoplasma virus
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                                                                                 Gene 141:1-8(1994).
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- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
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SIMILARITY: BELONGS TO THE SIGMA-54 FACTOR FAMILY.
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27; Conserv
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11 29 GLN
21 42 LEU
189 210 LEU
189 210 RPO
482 490 RPO
509 514 AKA
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32, Last annotation update)
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                                                                                                                                                                                               RNA stage; Plasmaviridae;
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Pred. No. 4.
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C291DAE1D2DD034C CRC64;
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LEUCINE-ZIPPER (POTENTIAL).
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   as long
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4.3;
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   its content
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                    no restrictions
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                                gh a collaboration EMBL outstation
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070695;
15-DEC-1998
15-DEC-1998
15-DEC-1998
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Hypothetical protein.
SEQUENCE 218 AA; 25564 MW;
                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                       EMBL; U94887; AAC40586.1; -.
Transferase; Nucleotidyltransferase; RNA-directed
SEQUENCE 1305 AA; 150293 MW; 321E9E7F3CF6F11A
                                                                                                                                                                                                                                                                                                                                                                                                                          sickness virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 98202706.
Vreede F.T., Huismans
"Sequence analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsRNA viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                African horse sickness virus 9 (AHSV-9) (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA-DIRECTED
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                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                                                                                     22 GRIDGTK--MYYEYYRYSSKMRETRRKKGTKYKTDDEFLERERDAGRLKLYDLQVIREAS 79
                                                                                                                              49 GRLDALREWIYYNYYTERSKRRDRRRRSVCHART--WFCFRKYD-----YVRRSI 96
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l Similarity 24.3%;
17; Conservative :
                                                                                                                                                         1 Similarity
19; Conserv
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(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
D RNA POLYMERASE (EC 2.7.7.48) (VP1).
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the RNA polymerase
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                                                                                                                                                         Score, 66; DB Pred. No. 20; 9; Mismatches
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CRC64;
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STANDARD;

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CARBOHYD
SEQUENCE
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"Cloning, expression and characterization of plasma platelet-activating factor-acetylhydrolase from guinea pig.";
J. Blochem. 120:838-844(1996).
1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
BY HYDROLYZING THE SN-2 ESTEN BOND TO YIELD THE BIOLOGICALLY
INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
RESIDUE AT THE THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D67037; BAA11054.1;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
15-FEB-2000 (Rel. 39, Last annotation update)
PLATELET ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Hystricognathi; Cavildae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P70683;
01-NOV-1997
                                                                                                                                      223
                                                                                                                                                                                                                          163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-HARTLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                             74 RRSVC-HARTW 83
                                                                                                                                                                                                                                                      22 LGVAYSAVVDVIRAAAHE-----GVYIEPEARGRLDALREWIYY---NYYTERSKRRDRR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN PHOSPHOLIPIDS.

CAPALTTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE
H(2)O-- 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.

SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: PLASMA.

SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                    RGEECSQALSW
                                                                                                                                                                                                                    IGIELASHGFIVAAVEHRDESAAATYYFQDAPAAESGNRSWIYYKVGNLETEERKRQLRQ 222
                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipid degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271
294
349
76
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Ą,
                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436
                                                                                                                                                                                                                                                                                                                                                                                                                        49062 MW;
                                                                                                                                                                                                                                                                                                                               10.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _SER; 1.
tion; Glycoprotein; Signal.
BY SIMILARITY.
PLATELET-ACTIVATING FACTOR
                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                          Pred. No. 6.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                             Score 65.5; D. Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
C359D96E392FFE11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACETYLHYDROLASE.
                         PRT;
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                                                                                                                                                                                                                                                                                                        32;
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                                                                                                                                                                                                                                                                                                                                                   Length 436;
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Matches
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NP_BIND
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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or send an email to license@isb-sib.ch).
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-!- FUNCTION: MOTOR FOR ANYEROGRADE AVONAL TRANSPORT OF SYNAP
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1;
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2;
PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X90840; CAA62346.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VESICLE PRECURSORS (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE KINESIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UTL-1998 (Rel. 36, Last annotation update)
KINESIN-LIKE PROTEIN KIFIA (AXONAL TRANSPORTER OF SYNAPTIC VESICLES).
 732
                                                                             673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 FHA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIFIA OR ATSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 96299637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                               53
                                                                                                                                                                                                                                                  Local
                                                                                                                                                                               7 PAPPV--CDSQNECVGWLGV-----AYSAVVDVIRAAAHEGVYIEPEAR----GRLD 52
FLKEANAISVELKKKVQ 748
                                   ---TTNTISVVSAHSVQ 114
                                                                         ALQKQMDSRYYPEVNEEEEEPPEDEVQWTERECELALW-AFRKWKWYQFTSLRDLLWGNAI 731
                                                                                                             ALREWIYYNYYTERSKRRDRRRRSV----
                                                                                                                                                 PAEPVDWAFAQRELLEKQGIDMKQEMEQRLQELEDQYRREREEATYLLEQQRLDYESKLE 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00225; kinesin; 1. PF00498; FHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                                                              l Similarity
32; Conserv
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366
429
516
622
801
1575
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383
462
572
681
822
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                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                            Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                            MW.
                                                                                                                                                                                                                                                                                                                                                                                FHA.
COILED
COILED
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Coiled coil
MECHANOCHEMICAL (MOTOR).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                ATP
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
D8DDEC784624FB4D CRC64;
                                                                                                                                                                                                                                                                64;
                                                                                                             -CHARTWFCFRKYDY-----VRRSIWHDT- 101
                                                                                                                                                                                                                                                                                                                                                                                COIL
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                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN FAMILY. UNC-104
                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                Length 1690;
                                                                                                                                                                                                                           Indels,
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793173; 061770;
01-0CT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last seq
15-JUL-1998 (Rel. 36, Last ann
KINESIN-LIKE PROTEIN KIFIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KF1A MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 95292344.

Okada Y., Yamazaki H., Sekine-Aizawa Y., Hirokawa N.;

"The neuron-specific kinesin superfamily protein KIFIA is a unique
"The neuron-specific kinesin superfamily protein KIFIA is a unique
"The neuron-specific kinesin superfamily protein KIFIA is a unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIF1A OR KIF1.
                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 93077686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY SEQUENCE OF 100-247
                                                                                                                                                                                            MGD; MGI:108391; KIFIA.

PRINTS; PR00380; KINESINHEAVY.

PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1;

PROSITE; PS50061; KINESIN_MOTOR_DOMAIN2;

PROSITE; PS50003; PH_DOMAIN; 1.

PROSITE; PS50006; FHA_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Kinesin family in murine central nervous system.";
J. Cell Biol. 119:1287-1296(1992).
-1- FUNCTION: MOTOR FOR ANTEROGRADE AXONAL TRANSPORT OF SYNAPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aizawa H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-BRAIN;
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                                                                                                                                                                                                                                                                                                                      EMBL; D29951;
                                                                           DOMAIN
                                                                                           DOMAIN
                                                                                                       DOMAIN
                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERINUCLEAR AND SYNAPTIC REGIONS.
SIMILARITY: BELONGS TO THE KINESIN-
SUBFAMILY:
SIMILARITY: CONTAINS 1 FHA DOMAIN.
SIMILARITY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VESICLE PRECURSORS.
SUBUNIT: MONOMER.
SUBUNIT: MONOMER.
TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY IN ADULT BRAINTISSUE (MAINLY IN THE CEREBELLUM AND CEREBRUM) WITHIN A SINGLE TYPE OF NEURONAL CELL. WITHIN THE NEURONAL CELL LEVELS ARE CONCENTRATED AROUND THE AXON, WITH SMALLER AMOUNTS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81:769-780(1995)
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                           Microtubules;
1 361
66 383
29 462
572
16 572
16 822
01 822
1678
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FHA; 1.
                                                                                                                                                                                   PH;
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36, Last annotation updat
EIN KIFIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takemura R., Zhang Z., Nangaku
   191724
                                            ; ATP-binding; Coiled coil.
MECHANCHEMICAL (MOTOR).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
FHA.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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   (BY SIMILARITY).
D6EC3B88CBC9CCC6 CRC64;
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Best Local Sim
Matches 32;
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Q61885; Q62003;
Q1-NOV-1997 (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
MYELIN-OLIGODENDROCYTE GIYCOPROTEIN PRECURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mamp
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mus.
                                                                                                                                              Amiguet P., Gardinier M.V., Zanetta J.-P., Matthieu "Purification and partial structural and functional of mouse myelin/oligodendrocyte glycoprotein.";
J. Neurochem. 58:1676-1682(1992).
-I-FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gardinier M.V., Matthieu J.M.;
"Murine and human MOG are highly conserved: cDNA analysis.";
Trans. Am. Soc. Neurochem. 24:234-234(1993).
                                                                                                                                                                                                                                                                               "Myelin/oligodendrocyte glycoprotein is a member of a immunoglobulin superfamily encoded within the major histocompatibility complex."; proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 29-246 FROM N.A. STRAIN-BALB/C; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daubas P., Pham-Dinh D., Dau
"Structure and polymorphism
glycoprotein gene.";
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Pontarotti P., Roeckel N., Mather I.H.,
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 93376728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                       STRAIN-BALB/C; TISSUE-BRAIN;
                                                                                                                                                                                                                                                      SEQUENCE OF 29-54
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                                                                                                                                                                                                                                                                                                                                      Dautigny A.;
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             MEMBRANES.
DISEASE: REDUCED CONCENTRATIONS OF MOG
DISEASE: REDUCED CONCENTRATION MICE.
OUACKING DYSMYELLNATING MUTANT MICE.
SIMILARITY: BELONGS TO THE IMMUNOGLOBUL
                                                                  SUBUNIT: MAY FORM HOMODIMERS.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIDECELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE
LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALREWIYYNYYTERSKRRDRRRRSV-----CHARTWFCFRKYDY-----VRRSIWHDT-
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                                                                                                                           CELL COMMUNICATION
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                                                                                                                                      COMPLETION AND/OR MAINTENANCE OF
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sm of the mouse
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Pred. No.
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ANCE OF THE MYELIN SHEATH AND
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                                          ARE OBSERVED
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characterization
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V-LIKE DOMAIN.

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069969;
15-DEC-1998
                                                                                                                                                                 Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
    This SWISS-PROT entry is copyright.
                                                                                        Seeger K.J., Harris D., Parkhill J., Barrell B.G., I Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databa-i- CATALYTIC ACTIVITY: LL-2,6-DIAMINOHEPTANEDIOATE
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                                                                 -!- PATHWAY: SIXTH STEP
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15-DEC-1998 (Rel.
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    SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
    SIMILARITY: BELONGS TO THE DIAMINOPINELATE EPINERASE FAMILY.

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PIMERASE (EC 5.1.1.7) (DAP EPIMERASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 93:4638-4643(1996).
-!- FUNCTION: MAY SERVE AS "FLIPPASE" AS WELL AS A GLUCOSYLTRANSFERASE
THAT TRANSFERS GLUCOSE TO CERAMIDE.
-!- CATALYTIC ACTIVITY: UDP-GLUCOSE + N-ACYLSPHINGOSINE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UL-1998 (Rel. 36, Last annotation update)
CERAMIDE GLUCOSYLTRANSFERASE (EC 2.4.1.80) (GLUCOSYLCERAMIDE 'SYNTHASE)
(UDP-GLUCOSE:N-ACYLSPHINGOSINE D-GLUCOSYLTRANSFERASE) (GLCT-1)
                                                                                                                                                                                                                                                                                                                                                                                                    -!- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED.
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Homo sapiens (Human).
Homo sapiens (Chordata)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ichikawa S., Sakiyama H., Suzuki G., Hidari K.I., Hirabayashi Y.; 
"Expression cloning of a cDNA for human ceramide glucosyltransferase that catalyzes the first glycosylation step of glycosphingolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Isomerase; Lysine biosynthesis.
ACT_SITE 85 85 BY SIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UDP + D-GLUCOSYL-N-ACYLSPHINGOSINE.
PATHWAY: FIRST GLYCOSYLATION STEP OF GLYCOSPHINGOLIPID SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN. ENDOPLASMIC
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289 AA;
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Matches 11
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"Plant 21D7 protein, a nuclear antigen associated with cell divisions a component of the 26 proteasome.";
"Plant Physiol. 113:281-291(1997).
"Plant Physiol. 113:281-291(1997).
"Plant Physiol. 113:281-291(1997).
"POUCTION: MAY PLAY A ROLE IN REGULATION OF THE 26S PROTEASOME ACCULTY IN RELATION TO CELL PROLIFERATION."
"INSUBCELLULAR LOCATION: NUCLEAR."
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Q06364;
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith M.W., Ito M., Yamada T., Suzuki T., Komamine A.; "Isolation and characterization of a cDNA clone for plant nuclear antigen 21D7 associated with cell division.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
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MEDLINE; 97161126
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SEQUENCE
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el. 37, Last annotation update)
REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7).
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55351 MW;
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                                                                  Mismatches
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                                                                                                                        Length 488
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EMBL; £15626; AAA16055.1;
EMBL; £28279; CAA82132.1;
PIR; S38128; S38128
SGD; L0000538; DYN1.
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01-JUN-1994
01-JUN-1994
15-FEB-2000
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Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetaceae; Saccharomyces.
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01-JUN-1994 (Rel. 29, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).
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MEDLINE; 94052110.
L1 Y.-Y., Yeh E.Y.,
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SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND INTERMEDIATE AND LIGHT CHAINS.
SUBCELLULAR LOCATION: CYTOPLASMIC. PROBABLY BINDS 1
THE INNER PLASMA MEMBRANE.
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"A conformational study of the human and rat encephalitogenic myelin oligodendrocyte glycoprotein peptides 35-55.";
Eur. J. Biochem. 246:59-70(1997).
-I- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
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immunoglobulin superfamily.",
J. Neurosci. Res. 33:177-187(1992).
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SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUDERFAMILY. CONTAINS ONE V-LIKE DOMAIN. BELONGS TO THE ETN/MOG SUBFAMILY.

CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)
                                                                                                                                                CELL COMMUNICATION.
SUBUNIT: MAY FORM HOMODIMERS.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
MEMBRANES.
                                                                                                    DEVELOPMENTAL STAGE: A PEAK OF EXPRESSION HAS BEEN OBSERVED BETWEEN POSTNATAL DAYS 15 AND 25, COINCIDENT WITH THE PERIO
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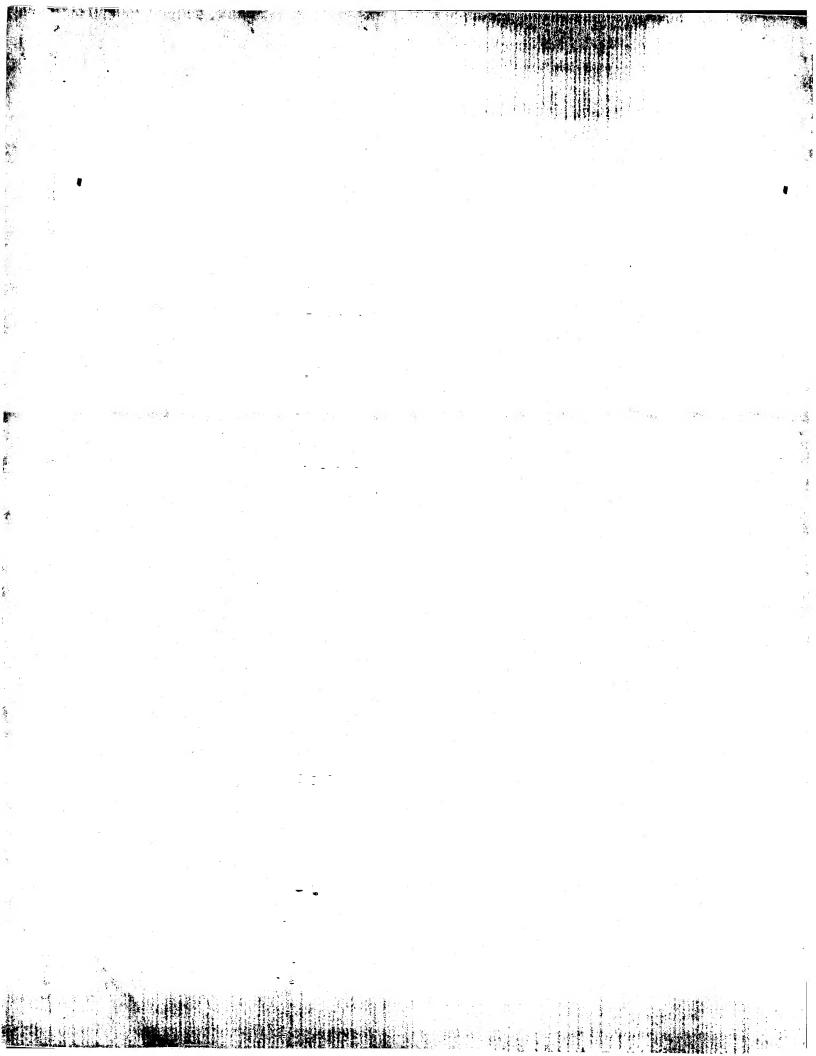
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## ALIGNMENTS

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**Sequence characterization

**YIrology 172:134-144(1989).
                                                                                                                                             PIENIAZEK N.J., SLEMENDA S.B., PIENIAZEK D., J
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ
EMBL; L19443; AAC13982.1; -.
SEQUENCE 121 AA; 13976 MW; 8B84054F CRC32,
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TOOGOOD C.I., MURALI R., BURNETT R.M., HAY R.T.;

"The adenovirus type 40 hexon: sequence, predicted relationship to other adenovirus hexons.";

J. Gen. Virol. 70:3203-3214(1989).
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DAVISON A.J., TELFORD
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Submitted (APR-1995) to the
EMBL; U24436; AAA66077.1;
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PFAM; PF01359; Transposase_
SEQUENCE 347 AA; 40758 M
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01-MAY-1999
                         Science 273:1058-1073(1996).
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Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Sciaroidea;
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SEQUENCE 123:
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ROUNSIEY S.D., LIN X., KAUL S., SHEA T.P., FUJII C.Y., MASON T.M.
SHEN M., RONNING C.M., FRASER C.M., SOMERVILLE C.R., VENTER J.C.
"Arabidopsis thaliana chromosome II BAC 76B13 genomic sequence."
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AC005398; AAC65978.1. -
SEQUENCE 945 AA; 108084 MW; 88791777 CRC32:
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudicotyledons; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
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       Orthopoxvirus [1]
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                                                                                                               Ectromelia virus
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PROTEIN.
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Pred. No. 4
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                                                                                   Poxviridae; Chordopoxvirinae;
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Best Local Similarity
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Q64304;
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01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-NOV-1998 (TREMBLREL. 08, Last annotation update)
PROTEIN LINKED TO SYSTEM L-LIKE NEUTRAL AMINO ACID
ACTIVITY.
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                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-SPRAGUE DAWLEY: TISSUE-JEJUNAL BRUSH BORDER;
YAO S.Y.M., MUZYKA W.R., CHEESEMAN C.I., ELLIOTT J.F., YAO S.Y.M., MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                     STRAIN-SPLAGUE-DAWLEY;
MEDLINE; 98395066.
KANAI Y., SEGAWA H., MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96128073.

MEDLINE; 96128073.

BROEER S., BROEER A., HAMPRECHT B.;

BROEER S., BROEER A., HAMPRECHT B.;

"The 4F2hc surface antigen is necessary for expression of like neutral amino acid-transport activity in C6-BU-1 rat cells: evidence from expression studies in Xenopus laevis Biochem. J. 312:863-870(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus leucopus (mottle-tailed rat), and Rattus norvegicus (R
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                 EMBL; X89225; CAA61509.1;
EMBL; U59324; AAC53560.1;
EMBL; AB015433; BAA33036.
PFAM; PF00128; alpha-amyl
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              SEQUENCE
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                                                                                                                                                                            KANAI Y., SEGAWA H., MIYAMOTO K., UCHINO H.,
Expression cloning and characterization of a
neutral amino acids activated by the heavy of
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                  Biol.
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                                                                                                                                                                       amino acids
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                alpha-amylase;
AA; 58072 MW;
                                                               BAA33036.1;
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65281 MW;
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.6%;
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                                                                                                                                                                                                                                                                        TISSUE-LIVER;
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Pred.
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1.
6C2869F1 CRC32;
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CHERNOS V.
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RESULT
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701-UN-1998 (Trembirel. 06, Created)
01-UN-1998 (Trembirel. 06, Last sequence update)
01-NOV-1998 (Trembirel. 08, Last annotation update)
HYPOTHETICAL 31.8 KD PROTEIN.
MIY036.18C.
                                                                                           Q9ZQ98 PRELIMINARY; PRT; 496 AA.
Q9ZQ98;
Q1-MAY-1999 (TIEMBLIFEL 10, Created)
O1-MAY-1999 (TIEMBLIFEL 10, Last sequence update)
O1-NOV-1999 (TIEMBLIFEL 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A STATE
Arabidopsis thaliana (Mouse-ear cress).
Eukkryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
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                                                                          PUTATIVE GLUCOSYL TRANSFERASE F13K3.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 284 AA; 31801 MW;
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EMBL; AL021931; CAA17389.1; -.
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PHILIPP W.J., POULET S., EIGLMEIER K.,
BALASUBRAMANIAN V., HEYM B., BERGH S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Myco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLE S.T., PARKHILL J., Submitted (FEB-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-H37RV;
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ilarity 29.5%;
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Pred. No. 16;
9; Mismatches
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Pred. No. 30;
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BLOOM B.R., JACOBS
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048839;
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Arabidopsis.
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                     PRELIMINARY;
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SEQUENCE FROM N.A.

CARTES A.C.;

Thesis (1998), University of Melbourne,
EMBL; AJ005690; CAA06674.1; -.

HSSP; P08631; 2HCK.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygil; Teleostei; Euteleostei; Ostariophysi; C
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,
CARRERA A.J., CREASY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,
FRASER C.M., VENTER J.C.;
"Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence.",
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006282; AAD20152.1; -.
EMBL; BS00375; UDPGT; 1.
                                                                                                                                                                                                                                                                                                     PFAM; PF00069; pkinase; 2.
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                                       65 ERSKRRDRRRRSVCHARTWFCFRKY 89
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                                                                                                                  5 ALPAPPVCDSQNECVGWLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIYYNYYT 64
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KNMREHIQNQHLVTRKRIRFRFRRF 213
                                                                               AVSVPVSLEFQEECLG-----LAVLDIMRLAKEKG--
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                                                                                                                                                                l Similarity
19; Conserv
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                                                                                                                                                                                                                                                              1095 AA; 125171 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TremBirel 08, Created)
(TremBirel 08, Last sequence update)
(TremBirel 12, Last annotation updat
OSINE KINASE (EC 2.7.1.112).
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                                                                                                                                                                                 Score 64.5;
Pred. No. 79;
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Pred. No. 31;
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                                                                             KSPVDIYNHSSYKSFLP 188
                                                                                                                                                              Indels
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Best Local
                                                                                                                                                                                                                                                      WATSON A., WEINSTOCK L.,
                                                                                                                                                                                                                                                                        WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY J., COUPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LICHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., MIKKEN L., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., WATERSTON R.,
WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
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SEQUENCE
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ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDC
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS N
SOMERVILLE C.R., VENTER J.C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC003974; AAC04485.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabldopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;

core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 94150718. WILSON R., AINSCOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-NOV-1996 (TIEMBLIEL. 08, Last annotation update)
SIMILARITY TO HUMAN FOLICULAR VARIANT TRANSLOCATION
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01-JUN-1998 (TrEMBLrel. 06,
01-MAX-1999 (TrEMBLrel. 10,
PUTATIVE UBIQUITIN SPECIFIC
                                                                                                                                                                                                                                   elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                  Submitted (FEB-1996)
                                                                                                                             SEQUENCE FROM N.A. BENTLEY D.;
                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q19843;
Submitted (FEB-1996)
                        WATERSTON
                                                SEQUENCE FROM N.A.
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18; Conserv
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Last sequence update)
Last annotation updat
PROTEASE.
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Pred. No. 88;
L2; Mismatches
EMBL/GenBank/DDBJ databases
                                                                                                EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                      J., WOHLDMAN P.; from chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPEARGRLDALREWIY 59
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Best Local (
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                                                  094512
094512;
01-MAY-1999
01-MAY-1999
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093370;
01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                           PRINTS; PR00
Paired box;
SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TREMBLIGE). 08,
01-NOV-1999 (TREMBLIGE). 12,
TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U49829; AAA93385.1; -. SEQUENCE 264 AA; 29808 MW;
PROBABLE INVOLVEMENT IN ERGOSTEROL BIOSYNTHESIS SPBC646.08C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                         Development 125:3063-3074(1998).
-!- SUBCELLULAR LOCATION: NUCLEAR
-!- SIMILARITY: CONTAINS A PAIRED
EMBL; AF072547; AAC31811.1; -.
HSSP; P06601; 1PDN.
PROSITE; PS00034; PAIRED_BOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygil; Teleostei; Euteleostei; Ostariophysi; C
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00292; PAX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFEFFER P.L., GERSTER T., LUN K., BRAND M., BUSSLINGER M.; "Characterization of three novel members of the zebrafish Pax2/5/8 family: dependency of Pax5 and Pax8 expression on the Pax2.1 (noi)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAX2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 98337826.
                                                                                                                                                                                                                 162
                                                                                                                                                                  220
                                                                                                                                                                                                                                                                                                                                                                                                                                                      unction.
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                                                                                                                                                                                       53 ALREWIYYNYYTER
                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                       2 VLPALPAPPVCDSQNECVGWLGVAYSAVVDVIR-----AAAHEGVYIEPEARGRLD 52
                                                                                                                                                                SLRKHLRADAFTQQ
                                                                                                                                                                                                                IIPSTASPPVSSSSNDPVG--SYSINGILGIPRSNGEKRKRDADGSEGSAQSSDSQGSVE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTPMILENNMRPTC---TWFPFMSIRSCSKRMVDSILKEKVHAFVPSYITLI 112
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                                                                                                                                                                                                                                                                l Similarity
16; Conserv
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box; DNA-binding; Developmental protein;
E 386 AA; 41541 MW; 5BCDF72B CRC32;
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                                                (TrembLrel. 10, Created)
(TrembLrel. 10, Last sequence update)
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                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                          10.2%;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                           Score 63.5;
Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                        Nuclear
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                                                                                                                                                                                                                                                                                                                                      protein
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Best Local Similarity
Matches 25; Conserv
                                                                                                            Query Match
                                                                            Matches
                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., TSCHUDY M.M., LIN X., KETCHUM K.A., CROSBY M.L.,
ROUNSLEY S.D., TSCHUDY M.M., MASON T.M., KETCHUM K.A., CROSBY M.L.,
SOMERTVILLE C.R., VENTER J.C.;
SUMMITTHE C.R., VENTER J.C.;
SUMMITTHE C.R., VENTER J.C.;
SUMMITTHE C.R., VENTER J.C.;
SUMMITTHE C.R., VENTER J.C.;
SUMMITTHE C.R., VENTER J.C.;
SUMMITTHE C.R., ARB64317.1;
PFAM; PF00556; TBC; 1.
SEQUENCE 756 AA; 85182 MW; F71F6CF4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                        022863;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL PROTEIN.
T01024.23.
                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viriddiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-972H-;
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355 WLWTLHRIVVDVVRTDSHLEFYEDPGNLGRMSDILAVYAWV 395
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                                    21 WLGVAYSAVVDVIRAAAHEGVYIEPEARGRLD---ALREWI 58
                                                                        Match 10.2%;
Local Similarity 34:1%;
hes 14; Conservative
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                                                                      Score 63.5; DB 10; Length 756; Pred. No. 66; 7; Mismatches 17; Indels 3
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Search completed: June 23, 2000, 10:07:48 ຊູງob time: 951 sec

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Maximum DB seq length: 1000000
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed;
and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Packfiles1.seq:*
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US-08-374-483-6
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US-08-379-452-43
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US-08-452-267-3
US-08-630-820-5
US-08-723-624-19
US-08-818-772A-2
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Sequence 28, Appl
Sequence 28, Appl
Patent No. 5432081
Sequence 14, Appl
Sequence 3, Appli
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Sequence 9, Appli
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09-4/c 1NOPRATION: INFORMATION: INFORMATION: ANT: Chamberlain, Jeffrey S. ANT: Hauser, Michael A. ANT: Hartigan-O'Connor, Denni OF INFORMATION: IMPROVED ADDROV OF SEQUENCES: 15: ESSEE: Medlen & Carroll, LLP EESSEE: Hand PC compatible OF ANTICON INFORMATION: ETAPLICATION NUMBER: US/08/735,609 EESSETICATION NUMBER: UM-02484 DEGENANTION INFORMATION: ESTRATION NUMBER: UM-02484 DEGENERATION INFORMATION: ESTRATION NUMBER: UM-02484 DEGENERATION INFORMATION: ESTRATION NUMBER: UM-02484 DEGENERATION INFORMATION: ETAPS: (415) 397-8338 ETON FOR SEQ ID NO: 4: CE CHARACTERISTICS: CHARACTERISTICS: CHARACTERISTICS: CHARACTERISTICS: CHARACTERISTICS: CHARACTERISTICS	26.6 7.7 2740 1 US-08-100-247 26.6 7.7 2740 2 US-08-232-513 26.6 7.7 2740 2 US-08-232-513 26.6 7.7 2740 2 US-08-232-63 26.4 7.7 2740 2 US-08-232-463 26.4 7.7 7218 1 US-08-232-463 26.2 7.6 34 US-08-572-126 26.2 7.6 1307 4 US-08-676-136 26.2 7.6 1307 4 US-08-676-146 26.2 7.6 1849 4 US-08-675-123 26.2 7.6 1849 4 US-08-675-132 26.2 7.6 1849 4 US-08-675-132 25.8 7.5 1320 5 US-08-751-233 25.8 7.4 1897 1 US-08-245-688 25.6 7.4 1897 1 US-08-245-688 25.6 7.4 1897 1 US-08-245-688 25.6 7.4 1897 1 US-08-245-688 25.6 7.4 1897 1 US-08-245-688
s J. IRUS VECTORS    ite 2200	A-4 Sequence A-5 Sequence A-6 Sequence Sequence A-14 Sequence -14 Sequence -17 Sequence A-1 Sequence A-1 Sequence -167 Sequence -167 Sequence -167 Sequence -167 Sequence -168 Sequence -169 Sequence
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Query Match Best Local Similarity Matches 345; Conserv

Conservative

100.0%; Score 345; DB 4; 100.0%; Pred. No. 2.3e-112; ... Mismatches 0;

Length 34303; Indels

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S-08-374-483-6
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                                   Matches
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REGISTRATION NUMBER: 1579
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 34382 base pairs
                                                        Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                        Local Similarity
les 345; Conser
                                                                                                                                                         TOPOLOGY: 11
                                                                                                                                                                                     LENGTH: 34382 base pairs
TYPE: nucleic acid
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 1 atggttcttccagctcttcccgctcctcccgtgtgtgactcgcagaacgaatgtgtaggt 60
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                                     100.0%; Score 345; DB 3;
100.0%; Pred. No. 2.3e-112;
tive 0; Mismatches 0;
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                                                                  Length 34382;
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                                   Gaps
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Query Match
Best Local Similarity
Matches 345; Conserv
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                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08735609
Patent No. 5955360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32243 ACGACCAACACGATCTCGGTTGTCTCGGCGCACTCCGTACAGTAG 32199
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                 MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
CORRESPONDENCE Medien & Carroll, LLP
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, S
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chamberlain, Jeffrey S. APPLICANT: Amalfitano, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hauser, Michael
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                                                               TOPOLOGY:
                                                                                  STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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VENTION: IMPROVED ADENOVIRUS VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States Of America
                                                               linear
                 /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/735,609
                                                                                                                                                                                                                                                                              UM-02484
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Conservative

100.0%; Score 345; DB 4; 100.0%; Pred. No. 2.3e-112; tive 0; Mismatches 0;

Length 35935; Indels

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                                                                                                                                                                          APPLICATION NUMBER: WO PCT/FR94/00624
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                            REFERENCE/DOCKET NUMBER: 0
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34042 ACGACCAACACGATCTCGGTTGTCTCGGCGCACTCCGTACAGTAG 33998
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPUTER: COMPUTER: PATENTIAN PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.
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CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: IMLER, Jean-Luc
PPLICANT: MEHTALI, Majid
PPLICANT: PAVIKANI, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Alexandria
STATE: Vir-
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08 FILING DATE: 26-JAN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States ZIP: 22314-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING COMPLEMENTATION LINES
                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                           : 35935 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                             US/08/379,452
                                                                                                                                                                 029395-002
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Best Local Similarity 100.0%;
Matches 345; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5756283
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                                                                       TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 8299 base pairs
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CITY: Spring F
CITY: PA
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
APPLICANT: Gao, Guang-Ping
TITLE OF INVENTION: Method for Improved Production of
TITLE OF INVENTION: Recombinant Adeno-Associated Viruses
                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,
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                                                                                                                                                          REFERENCE/DOCKET NUMBER: UP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/O FILING DATE: 05-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                   TOPOLOGY:
                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19477
                                                      nucleic acid
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Spring House Corporate Cntr., P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                       unknown
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                                          double
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Pred. No. 2.3e-112;
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33283 AGTTGGATGACTGAGCGGCAGCAGCGAAAGGACGGCCGCAGGAGGGGTATATGCTGTTCA 33224

aactactacacagagcgatctaagcggcgagaccggagacgcagatctgtttgtcacgcc 240

33343 TTTTTTATTTCATCAGATGCAGAGGAACTTCTCCAGAATCTTCGAGAATGGATGTACTTC 33284

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Best Local Similarity
                                                                                                                                                                                         Matches 145; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 35081 base pairs
TYPE: nucleac acid
STRANDEDNESS: single
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NAME: Seide, Rochelle K
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: A313
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212_705-5000
                                                                                                                 33460 ATGGTTCTTCCAATCCTGCCACCGCCCCCTCTGAATGATAGAC---AAGGCAGCATTAAC 33404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 20-NOV-19
121 gtttacatagaacccgaagccaggggcgcctggatgctttgagagagtggatatactac 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P.
STREET: 30 ROCKefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3462 CGGCGCACTCCGTACAGTAG 3481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPONENTING SYSTEM:
                                                                                                                                               1 atggttcttccagctcttcccgctcctcccgtgtgtgactcgcagaacgaatgtgtaggt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
IOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                             tggctgggtgtggcttattctgcggtggtggatgttatcagggcagcggcgcatgaagga 120
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Smith, Alan E.
Smith, CHIMERIC ADENOVIRAL VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                               212-705-5020
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                                                                                                                                                                                                                                                                                             linear
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20-NOV-1996
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100.0%; Pr
0;
                                                                                                                                                                                                         15.7%;
                                                                                                                                                                                  Score 54; DB 3; Length 35081;
Pred. No. 7e-09;
0; Mismatches 130; Indels
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Pred. No. 1.8e-18;
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US-08-452-267-2
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                                                                                                                                                                                                                                          Query Match
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LENGTH: 2633 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                 1071 CGCATGTCGCGCAAGACTGTAACCACGCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTG 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,267
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
1191 GCGGGACTTTGCAAGTGGTGA 1211
                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                           83 cggtggtggatgttatcagggcagcgcatgaaggagtttacatagaacccgaagcca 142
                                                                                                                                                      23 ctcctcccgtgtgtgactcgcagaacgaatgtgtaggttgggctggggtgtggcttattctg 82
                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Breen, John P.
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 66
                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                gggggcgcctggatgctttga 163
                                                                ATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTA 1190
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                                                                                                                                                                                                                       Similarity
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11 South Meridian
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Pred. No.
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                       1.3;
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Best Local Similarity 50.4%;
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                                                                                                                                           Patent No. 60080
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SEQUENCE CHARACTERISTICS:
LENGTH: 3035 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: BTIF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPAX: 512/474-7577
                                                                                                                          SENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: CONCULTENTLY HEREWITH
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                               1795 CGCATGTCGCGCAAGACTGTAACCACGCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTG 1854
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING THE EXPRESSION OF GENES IN PLANTS
                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                       143 gggggcgcctggatgctttga 163
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                                                         BOSSLET, Klaus
CZECH, Joerg
                                                                                                         Martin
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US-08-723-624-19

Patent No.

GENERAL INFORMATION: APPLICANT: Rose,

Rose, Alan B. Last, Robert L Sequence 19,

Application US/08723624

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US-08-630-820-5
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INFORMATION FOR SEQ ID NO:
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/630,820 FILING DATE: 10-APR-1996 PRIOR APPLICATION DATA: DE 19513676.4
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Foley & L
                                                               1984 ATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTA 2043
                                                                                                                                   1924 CGCATGTCGCGCAAGACTGTAACCACGCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTG 198
                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY:
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IMMEDIATE SOURCE:
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LENGTH: 3169 base pairs
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ATTORNEY/AGENT INFORMATION:
2044 GCGGGACTTTGCAAGTGGTGA 2064
                                  143
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CITY: Washington
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                    y Match 8.4%;
Local Similarity 50.4%;
hes 71; Conservative
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                                                                                                                                                       23 ctcctcccgtgtgtgtgactcgcagaacgaatgtgtaggtttggcttgggttgtggcttattctg 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: cir
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LOCATION: 3..641
                                                                                             cgqtggtggatgttatcagggcagcggcatgaaggagtttacatagaacccgaagcca 142
                            gggggcgcctggatgctttga 163
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202)672-5399
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666..3162
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                                                                                                                                                                                                      Score 29; DB 5;
Pred. No. 1.5;
0; Mismatches 7
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US-08-723-624-19
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                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                            APPLICANT: Ramsay, Nichola TITLE OF INVENTION: Control NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                                                                               2704 GCGGGACTTTGCAAGTGGTGA 2724
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NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
                                                                                                                                                                                                                                                                                                                                                                                                                                        2644 ATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTA 2703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2584 CGCATGTCGCGCAAGACTGTAACCACGCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTG 2643
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LENGTH: 3824 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: BT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 cggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacccgaagcca 142
                                                                    ZIP: 46204
                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 ctcctcccqtqtqtqactcgcagaacgaatgtqtaggttggctgggtgtggcttattctg 82
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                Indianapolis
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11 South Meridian
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50.48;
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Pred. No. 1.6;
0; Mismatches
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Query Match
Best Local Similarity
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                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC/AT
COMPUTER: IBM PC/AT
OPERATING SYSTEM: DOS Vers
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08318772A
Patent No. 5679558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-318-772A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (317) 231-745
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPULLULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             NERAL INFORMALL...

APPLICANT: GOBEL, Elke
APPLICANT: NAKAKIDO, Fumio
TNUFNTION: Transformation of monocot cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1126 ATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTA 1185
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IMMEDIATE SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
                                                                                                                                                                                                                                                                                        STREET: B1RCH, STEWART, KOLASCH & BIRCH STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                    APPLICATION NUMBER: PCT/EP93/00905
FILING DATE: 14-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 gggggcgcctggatgctttga 163
APPLICATION NUMBER: EP 92401066.3 FILING DATE: 15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 cggtggtggatgttatcagggcagcggcatgaaggagtttacatagaacccgaagcca 142
                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Breen, John P. REGISTRATION NUMBER: 38,833
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                                                                                                                                                                                DOS version 3.3
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Gaps 82

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SEQUENCE CHARACTERISTICS:
LENGTH: 5642 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1916 ATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTA 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1856 CGCATGTCGCGCAAGACTGTAACCACGCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTG 1915
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                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                            CURRENT APPLICATION DATA:
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TELEX: 248345
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les 71; Conserv
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TOPOLOGY: c1
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                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                     CITY: Seattle
                                                                                                                                                                                                                      STREET:
           APPLICATION NUMBER: FILING DATE: 25-JUI
                                                                                                                                                                                                                                     ADDRESSEE:
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R INFORMATION:
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                                                                                                                                                     98104-7092
                                                                                                                                                                                     Washington
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                                                                                                                                                                                                                      6300 Columbia Center,
                                                                                                                                                                        USA
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                                                                                                                                                                                                                                             SEED and BERRY LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double stranded
25-JUN-1997
N: 435
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                                                                                                                                                                                                                                                                                                                               Katherine J.
                                                                                                                                                                                                                                                                                           GLUCURONIDE REPRESSORS AND USES THEREOF
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1285 - 3093: coding sequenc
3094 - 3378: 3' regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-DNA nopaline synthase gene
3379 - 5642: pUC18 derived sequence
ampicillin resistance to the bacterium
                             US/08/882,704A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 - 3093: coding sequence of -glucuronidase gene
4 - 3378: 3' regulatory sequence containing the
yadenylation site derived from Agrobacterium
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                                                                                                                                                                                                                          701 Fifth Avenue
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
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     STRANDEDNESS:
                                                                                                          TELEPHONE:
                                     ENGTH:
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Sequence 1, Application US/08819866 Patent No. 5830698
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                     TELEFAX: (703) 836-202
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2097 ATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTA 2156
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                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               APPLICATION NUMBER: US/06
FILING DATE: 14-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS TITLE OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 gggggcgcctggatgctttga 163
                                                                                                                              TELECOMMUNICATION INFORMATION:
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REGISTRATION NUMBER:
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Local Similarity 50.4%;
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STRANDEDNESS: single
                                                                                                                                                   NAME: Teskin, Robin L. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States ZIP: 22313-1404
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: BURNS, DOANE, SWECKER & MATHIS, L.L.P. P.O. Box 1404
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BARNETT, Richard Spence
MCLACHLAN, Karen Retta
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                                                                                                           (703) 836-6620
                                                                                      836-2021
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                                                                                                                                                                          35,030
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Pred. No. 2.4;
0; Mismatches
                                                                                                                                                            012712-352
                                                                                                                                                                                                                                                                                                                                      Version #1
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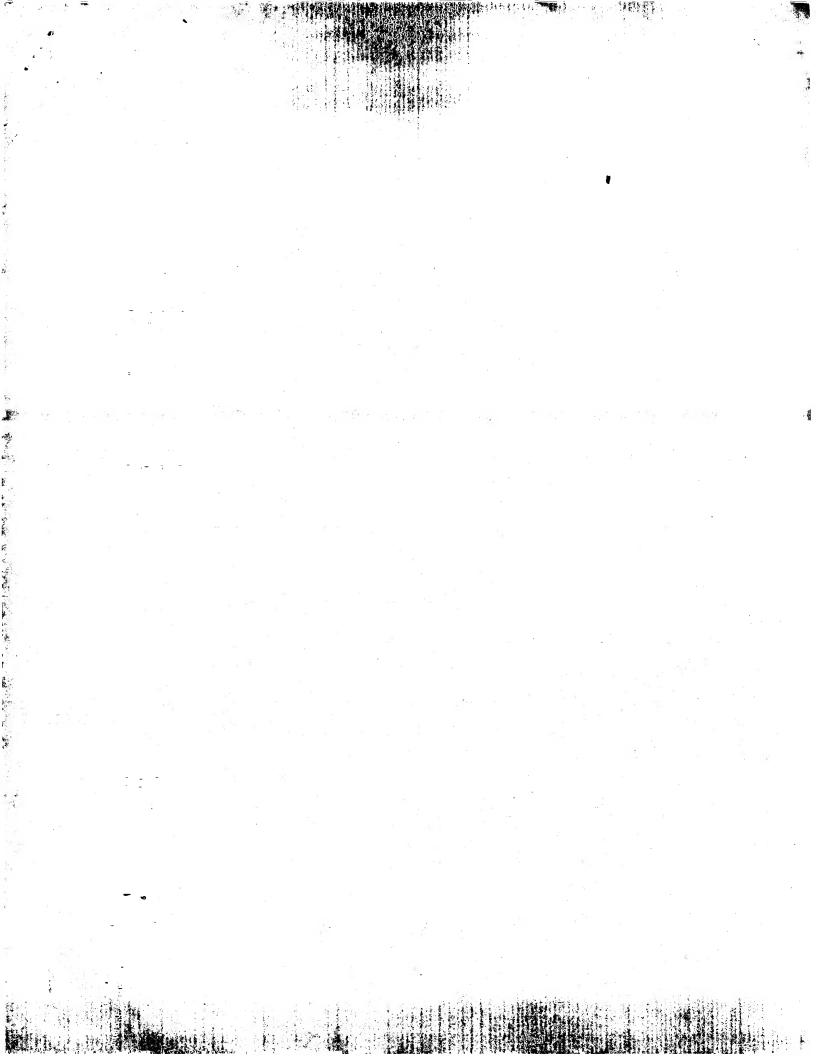
US-08-819-866-1

DNA (genomic)

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US-09-023-715-1/c
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                                                                                        MOLECULE TYPE:
            Matches.
                           Query Match
Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                 TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/819,866
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentinaRelease #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
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TOPOLOGY: 11
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            Conservative
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MCIACHIAN, Raten Retta
VENTION: RETHOD FOR INTEGRATING GENES AT
VENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
VENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
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Pred. No. 3.4;
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GCGGGACTTTGCAAGTGGTGA 7429
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Search completed: June 23, 2000, 09:51:55 Job time: 6701 sec



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protein 9 ::

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Title: US-09-214-478-4

Sequence: 1 MVLPALPAPPVCDSQNECVG.......SIWHI

Seriect score: 1 MVLPALPAPPVCDSQNECVG......SIWHI

MINIMUM DB seq length: 0

Maximum DB seq length: 1000000
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132.364 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Human cancer-relat
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Protein encoded by
Mouse protamine 1
Homo sapiens PSP1
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IGG-Fc binding pro-
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BtI109P insecticid
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Heavy chain variab
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Matches 27
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N-PSDB; N81266.

Cloned rhizobium meliloti ntrA gene - for use in C4-dicarboxylate cloned rhizobium meliloti, symbiotic nitrogen fixation and identifying pathogenic genes.

Claim 1; Page 12; 19pp; English.

The ntrA gene product is a transcriptional activator. It controls processes of nitrate assimilation, symbiotic nitrogen fixation and C4-dicarboxylate transport, working in conjunction with NtrC, NifA carboxylate transport, working in conjunction with NtrC and C4-dicarboxylate transport, working in conjunction with NtrC and C4-dicarboxylate transport, working in conjunction with NtrC and C4-dicarboxylate transport as the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state o
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13-JUN-1996;
15-JUN-1995;
                                                                                                                  Human ceramide glucosyltransferase.
Ceramide glucosyltransferase; GlCT-1; glycosphingolipid biosynthesis; glycosylation; glycosphingoceramide; glucosylceramide; human.
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Sequence 523 AA;
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29-MAY-1987; US-055228.
(GEHO-) Gen Hospital Corp
Ronson C, Ausubel F;
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W09088;
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pathogenesis.
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13-JUN-1996; 109447.
15-JUN-1995; JP-148472.
(RIKA ) INST PHYSICAL & CHEM RES
                                                                                Homo sapiens.
EP-748868-A2.
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nif operon; C4-dicarboxylate transport.
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Translation of TEV
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Human secreted pro
HindIII-EcoRl inse
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08-SEP-1998; U18638.

22-SEP-1997; US-059725.

08-SEP-1997; US-059180.

(UTPR-) UNIV PRINCETON.

Cong J, Schenk T, Zhu H;

WPF; 99-243729/20.
                                   New isolated human genes
Claim 5; Page 174-176; 184pp; English.
This sequence is encoded by a human gene of the invention, repressed in the presence of the recoded by a human gene of the invention, repressed in the presence of HCMV infection, designated HCMV-repressible genes (orgor crgs). The invention also relates to genes that are induced to express by both HCMV and interferon (IFN), designated HCMV-inducible genes (cig or cigs). The products can be used to obtain agents which can be used for anti-viral therapy, particularly anti-HCMV therapy. They can also be used for the development of drugs that would allow for higher dosage IFN treatments without the concomitant toxicity normally associated with administering high levels of IFN. The products can also be used for administering high levels of IFN. The products can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a novel ceramide glucosyltransferase (GlcT-1), which has catalytic activity for glucose transfer from UDP-glucose to ceramide. Ceramide glucosyltransferase catalyses the first glycosylation step of glycosphingoceramide to produce glucosylceramide, a precursor to more than 300 glycosphingolipid biosyntheses. The sequence can be used in biochemistry and biotechnology areas as laboratory agents, and also as preparatory agents. For the manufacture of pharmacological active substances. It is expected to have use in therapeutic and preventive treatment of glassess: based on reduced expression of ceramide
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HCMV repressible gene; crg; human; human cytomegalovirus; interferon; HCMV therapy; detection; diagnosis;
                                                                                                                                                                                                                                                                                  N-PSDB; X33956.
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WPI; 97-036152/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 MVFF-----MCHCLAWFIFDYIQLRGVQGGTLCFSKLDYAVAWFIRESMTIY 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 YNYYTERSKRRDRRRRSVCHARTWF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LPAPPVCDSQNEC-----VGWLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----IWHDT 100
                               for detection, diagnosis and drug screening
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Query Match Best Local Similarity

10.1%;

Score Pred.

No.;

DB 14;

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Length 394;

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Best Local
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                                     IgG-Fc binding protein.
Fragment 13; pNV11-ST; IgG-Fc binding human; colonic epithelium; monoclonal
                                                                                                                                                                                                                                                                                                                                                                                  DNA derived from colonic epithelium encoding IgG-Fc binding protein used in the mapping and analysis of IgG-Fc binding protein mRNA claim 1; Page 71-84; 132pp; Japanese.

This sequence is encoded by fragment 13 which is a NotI/KpnI fragment from pNVII-ST. This sequence represents a portion of the IgG-Fc binding protein of human colonic epithelium. This sequence was used in the isolation of the full length sequence given in WI4/49. mRNA isolated from human colonic epithelial tissue was used to prepare a cDNA library. This was screened using monoclonal antibodies K9 and K17 which bind to the large and small components of the binding protein. Pactive clones, see also T63077-81, were used to derive probes for screpning a second DNA library from human colonic epithelial tissue.
                                                                                                  W14749 standard; Protein; W14749;
            Homo sapiens.
WO9527057-A1.
                                                                                                                                                                                            1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IgG-Fc binding protein encoded by 7.8 kb fragment of pNV11-ST. Fragment 13; pNV11-ST; IgG-Fc binding protein; immunoglobulin; human; colonic epithelium; monoclonal antibody; K9; probe.
                                                                    13-MAY-1997 (first entry)
IgG-Fc binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 95-358632/46.
N-PSDB; T63073.
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03-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
WO9527057-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W14748;
13-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harada N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-AUG-1994;
30-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHUS ) CHUGAI SEIYAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W14748 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 IFLSALWDPT
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                                                                                                                                                                                                                                                                   ALPAPPVCDSQNECV------GWLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREW 57
                                                                                                                                                                                                                     IYYNYYTERSKRRDRRRRSVCHA
                                                                                                                                                                                                                                                  ALSAPPQC -- QDGCAEGCQCDSGFLYNGQACVPIQQCGCYHNGVYYEPEQTVLID----- 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----IWHDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPAPPVCDSQNEC-----VGWLGVAYSAVVDVIRAAHEGVYIEPEARGRLDALREWIY 59
                                                                                                                                                                                                                                                                                                            Similarity 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morikawa M;
                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP-129487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP-109927
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                                                                                                                                                                                         -NCRQQCTCHA 1613
                                                                                                                                                                                                                                                                                                                           10.1%;
27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MCHCLAWFIFDYIQLRGVQGGTLCFSKLDYAVAWFIRESMTIY 362
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                                                                                                                 5405
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                                                                                                                                                                                                                                                                                                         Score 62.5; DB 1;
Pred. No. 1.6e+02;
7; Mismatches 26;
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                                      protein; immunoglobulin;
antibody; K9; probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin; K17;
                                                                                                                                                                                                                                                                                                                                      Length 2594;
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New modified butyrophilin - not cross-reactive with myelin proligo-dendrocyte glycoprotein, useful in dairy products, vaccines, pr and assays for susceptibility to multiple sclerosis

PT and assays for susceptibility to multiple sclerosis

PT and assays for susceptibility to multiple sclerosis

PT and assays for susceptibility to multiple sclerosis

PT and assays for susceptibility to multiple sclerosis

PT and assays for susceptibility to Miltiple sclerosis

PT and assays for susceptibility product of the miltiple sclerosis (MS). The invention provides methods of the modifying BTN to eliminate sequences that elicit this immune component to MGG, e.g. by removing or modifying the Igi domain of a CC non-human BTN (nbBTN) in a ddary product, or by producing a numanised chimeric BTN. The invention includes genetic manipulation CC of the endogenous BTN gene of an animal such that the human Igi CC domain is introduced into the germiline of the animal, and the CC uncertage and for identify susceptibility to MS in a human patient from the provides of an animal and the development of the primary and the susceptibility to MS in a human patient from the primary and the susceptibility to MS in a human patient from the primary and the susceptibility to MS in a human patient from the primary and the susceptibility to MS in a human patient from the primary and the susceptibility to MS in a human patient from the primary and the susceptibility to MS in a human patient from the primary and the susceptibility to MS in a human patient from the primary and the susceptibility to MS in a human patient from the primary and the susceptibility to MS in a human patient from the primary and the susceptibility to MS in a human patient from the primary and the primary and the primary and the primary and the primary and 
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W97817
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA derived from colonic epithelium encoding IgG-Fc binding protein used in the mapping and analysis of IgG-Fc binding protein mRNA Claim 3; Page 86-113; 132pp; Japanese.

This sequence represents the IgG-Fc binding protein of human colonic epithelium. This sequence was isolated using the sequence given in w14748. mRNA isolated from human colonic epithelial tissue was used to prepare a cDNA library. This was screened using monoclonal antibodies K9 and K17 which bind to the large and small components of the binding protein. Active clones, see also T63077-81, were used to derive probes for screening a second DNA library from human colonic epithelial tissue. Sequence 5405 AA;
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Harada N, MOIlkawa M;
WPI; 95-358632/46.
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01-APR-1994; JP-129487.
24-AUG-1994; JP-222547.
30-MAR-1995; JP-109927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multiple sclerosis; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Linington C, Mather IH; WPI; 99-142845/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W97817 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUL-1997; US-053376.
(UXMA-) UNIV MARYLAND E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALSAPPQC -- QDGCAEGCQCDSGFLYNGQACVPIQQCGCYHNGVYYEPEQTVLID---
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Pred. No. 4e+02;
7; Mismatches
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k. Methods are
human patient from
risk of developing
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Best Local S
Matches 15
                                                                                                                                                     03-SEP-1998.
27-FEB-1998; 008258.
10-JUL-1997; DE-029490.
28-FEB-1997; DE-008134.
(EVOT-) EVOTEC BIOSYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a pathogenic autoimmune resp
possible, by screening the p
gene with domains which are
agonists or antagonists
Claim 3; Page 6-11; 21pp; German.
This sequence represents a head activator binding protein isolated from Chlorohydra viridissima by chromatographic methods. The protein is used in a screening assay for agonists or antagonists comprising determining the binding properties of candidate substances with the protein. The assay can be used to screen for substances useful for treating neurodegenerative diseases.

Sequence 1661 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydra head activator binding protein. Head activator binding protein; hydra; screening antagonist; treatment; neurodegenerative disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domains (claimed).
Sequence 150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlorohydra
                                                                                                         Hydra head activator binding protein - useful in screening assay for
                                                                                                                                Hampe W, Schaller C;
WPI; 98-468562/41.
                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
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                                                                                                                      N-PSDB; V46335
                                                                                                                                                                                                                    DE19808258-A1
                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                           BIOSYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label
                                                                                                                                                                                                                                                                /note= "As given in specification"
1368. .1543
                                                                                                                                                                                                                                                                                                                                                                        /label= vps10
/note= "As given
                                                                                                                                                                                                                                                                                         'label-
                                                                                                                                                                                                                                                                                                               note- "EGF-like region as given in
                                                                                                                                                                                                                                                                                                                                                                                                                                      note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label≖ signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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003 . . 1041
                                                                                                                                                                                                                                                                                                                                                                                                               label-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding protein.
ng protein; hydra; screening assay; agonist;
                                                                                                                                                                                                                                                                                                                                                               .1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                             l= head_activating_binding_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    "protease site"
                                                                                                                                                                                                                                                  "Fibronectin type III"
                                                                                                                                                                                                                                                                                                                                                                                                               N-terminus
                                                                                                                                                                                                                                transmembrane
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; Pred. No. 5.8;
5; Mismatches
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Query Match
Best Local Similarity
Matches 21; Conserv

Conservative

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Score 61.5; DB 1; Pred. No. 1.2e+02; 4; Mismatches 25

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize dwarf mosaic virus polyprotein. MDMV-B; viral resistance; disease res
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843
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/note= "portion of the helper component-P2
proteinase"
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'note= "conserved motif characteristic
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iote= "claimed polypeptide (Claim 20)"
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note= "claimed polypeptide (Claim 20)"
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Y viral protein

Scalaim 20; Page 31-44; 64pp; English:

The sequence of the polyprotein encoded by the polycistronic mRNA

C (T47073) of maize dwarf mosaic virus strain B (MDMV-B) is given in

CC W10344. New chimaeric genes comprise a monocotyledonous plant

CC promoter linked to a modified nucleic acid sequence derived from

CC the MDMV-B genome. The modification is such that mRNA is translated

CC to a truncated protein (pref. smaller than 200 amino acids), no

CC translation of mRNA occurs or the transcribed mRNA lacks the

CC translation initiation codon or includes a premature stop codon.

CC Expression of the chimaeric gene inhibits infection of plants (pref.

CC sorghum, sugarcane, esp. maize) by MDMV. The transgenic plants

CC display an inheritable resistance trait.
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                                                                        N-PSDB; Q23349.

Synthetic specific binding agent and reshaped human specific for human polymorphic epithelial mucin for in-vivo diagnosis of PEM-producing cancers Claim 11; Fig 12; 62pp; English.

The reshaped antibody sequence was deduced from the
                                                                                                                                                                  Verhoeyen M;
WPI; 92-114305/14.
                                                                                                                                                                                                                 W09204380-A.
19-MAR-1992.
05-SEP-1991; G01511.
07-SEP-1990; GB-019553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1992 (first entry)
Anti-bdy produced from HuVHlconHMFG1
Anti-HMFG specificity; complementari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-1997.
20-JUN-1996;
30-JUN-1995;
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        The reshaped antibody sequence was deduced from the sequence of a reshaped human variable heavy chain gene which had a human class; framework but contained mouse CDRs. To reshape a human heavy chait three fragents, each one contg. a murine CDR, were assembled to form gene HuVHIconHMFGI. The reshaped gene was inserted into a new yearter to produce a place of for transformer of a cold
                                                                                                                                                                                                                                                                                                                                                            protein
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N-PSDB; T47073.
Chimaeric gene for imparting
sequence modified to express
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produce a plasmid
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Pred. No. 2.
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Matches 23
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                                                                                                                                                                                                                                                                                                                                                                                                    - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The antibodies produced are essentially human so are unlikely to cause adverse reactions. The reshaped molecule can be used to treat PEM-producing cancers (e.g. of the breast, ovary, uterus or lung) and in in-vigo diagnosis.

See also R22419-22.

Sequence 118 AA;
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Esingle chain Fv fragment; ScFv; Gene Therapy; Monoclonal Antibody;
Human Milk Fat Globule antigen; HMFGl.
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97
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118
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87
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                1. .118
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23.2%; Pred. No.
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                    monoclonal antibody
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Best Local Similarity
Matches 23; Conserv
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04-NOV-1993;
04-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virus with modified binding molety specific for the target cells used to deliver genes for gene therapy and cancer treatment Example 4; Page 74; 110pp; English.

R54758 showes an humanised HMFGI heavy chain variable region. The mouse HMFGI is changed at specific residues within the framework region. It is used to generate an SCFV with the humanised HMFGI light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMCR ) IMPERIAL CANCER
Epenetos AA, Spooner RA
WPI; 94-167477/20.
N-PSDB; Q64819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                   Human secreted protein encoded by 5' EST SEQ ID NO: 142.
Human secreted protein; EST; expressed sequence tag; djagnosis;
forensic; gene therapy; chromosome mapping; signal peptide;
upstream regulatory sequence; cytokine activity; cell proliferation;
differentiation; haematopolesis regulation; tissue growth regulation;
reproductive hormone regulation; chemokarctic; chemokanetic; haemostati
thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9410323-A
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(GEST ) GENSET.

Duclert A, Dumas Milne Edwards J, Lacroix B;

WPI; 99-153782/13.

N-PSDB; X51928.

New isolated brain-derived nucleic acids - used to develop per the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state o
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The invention is concerned with the fusion fibre such that the fusion sequence can be
                                                                                                                                                                                                               31-JUL-1998; IB1236
01-AUG-1997; US-905:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y13128 standard; Protein; 133
                                                                                                                                                                                                                                                                                       WO9906552-A2.
                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRRDRRRRSVCHARTWFCFRKYDYVRRSIWHDTTINTIS 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                 US-905223
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108. .118
/label= FR 4
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31. .35
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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  sequence tags (ESTs) for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of an SCFv with the Ad5 used to target cells for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                products
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                                                                                                                                                                                                                                                                                                                                                              haemostatic;
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC secreted proteins, and encode the proteins given in x12987 to x13219, CC respectively. The proteins given represent the signal peptide and an CC N-terminal fragment of a secreted protein. The nucleic acid sequences CC can be used for producing secreted human gene products. They can also CC be used to develop products for diagnosis and therapy. The proteins CC obtained may have cytokine activity, cell proliferation/differentiation CC activity, heamatopoiesis regulating activity, tissue growth regulating CC chemokinetic activity—haemostatic and thrombolytic activity, receptor/CC ligand activity, anti-inflammatory activity, tumour inhibition activity cor other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or Sequence 133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-1998.
26-AUG-1997; 306501.
13-DEC-1996; US-032875.
06-SEP-1996; US-025436.
25-OCT-1996; US-027873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....W56767; standard; .....W56767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHomo sapiens PSP1 partial sequence.
PS-1; presentlin; presentlin-1; PSP-1; Alzheimer's disease; serine protease; neurodegeneration; predisposition; diagnos
                                                                                                                                                                  N-PSDB; V29522.

Nucleic acids encoding human serum protease protein(s) - used idagnosing pre-disposition to Alzheimer's disease, etc. Example 2; Page 18-19; 65pp; English.

The sequence is that of at least a fragment of the serine protease PSP1. This can be used to identify modulators of serine protease activity and also to diagnose a condition associated with lack of one of the serine proteases or a genetic predisposition to neurodegeneration in a patient, preferably predisposition to Alzheimer's disease.

Sequence 323 AA;
                                                                                                                                                                                                                                                                                                                                                                         (SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
BYOMNE MJ, Clinkenbeard HE, Creat-
Livi GP, Southan CD;
WPI; 98-161101/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
EP-828003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l3-OCT-1998 (first entry)
   77
                                                                         Local Similarity 32.0 ies 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                               2 VLPALPAPPVCDSQNECVGWLGVAYSAVVDVIRAAAHEGVYIE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 YAYHVEREKERDPEHRALCDLGPW 55
VLAAVPSPPPASPRSQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 323
                                                                                         9.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                Creasy CL,
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(20
                                                                                         Score 60;
Pred. No.
YNFIADVVEKTAPAVVY IE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60; DB
Pred. No. 8.6;
                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predisposition; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                Karran
                                                                                                           DB 1;
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                                                                       13; Indels
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                                                                                                         Length 323;
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Best Local Similarity 32.6
Matches 14; Conservative
                                  New polypeptide(s) involved in cobalamin and cobamide biosynthesis - and DNA encoding them, for amplification of cobalamin, esp. coenzyme B12 prodn, (Claim 17; Fig 16; 299pp; French.

This sequence corresponds to one of 24 polypeptides obtained from p. dentrificans and implicated in the biosynthesis of cobalamines and/or cobamides, specifically in catalysing the transfer of a methyl group to positions C1, C5, C11, C15 or C17 in the conversion of precorrin-3 to cobyrinic acid a, c-diamide. It is encoded by part of the 8.7kb EcoRI-EcoRI fragment of plasmid pXL367. The plasmid was isolated from a P. denitrificans genomic DNA bank constructed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-1998.
26-AUG-1997; 306501.
13-DEC-1996; US-032875.
06-SEP-1996; US-025436.
25-OCT-1996; US-027873.
                                                                                                                                                                                                                                                              Blanché F, Meron B, Crouzet J, Debussche L, Levy-Schil
                                                                                                                                                                                                                                                                                                                                                                            P.denitrificans COB L. cob gene; corrinoid; descobaltocorrinoid; cor
                                                                                                                                                                                                                                                                                                                                                                                                            R13506 standard; Protein; 413
R13506;
25-OCT-1991 (first entry)
              vector pXL59.
See Q13284-Q13288.
                                                                                                                                                                                                                      N-PSDB; Q13285.
                                                                                                                                                                                                                                                      Thibaut D
                                                                                                                                                                                                                                                                                                   30-JAN-1991; F00054.
31-JAN-1990; FR-001137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; v29537.

Nucleic acids encoding human serum protease protein(s) - us diagnosing pre-disposition to Alzheimer's disease, etc. claim 7; Page 41-42; 65pp; English.

The sequence is that of the consensus sequence of PSP1-3 serine protease which can be used to identify modulators of serine protease activity and also to diagnose a condition associated with lack of one of the serine proteases or a genetic predisposition to neurodegeneration in a patient, preferably predisposition to Alzheimer's disease.

Sequence 377 AA;
                                                                                                                                                                                                                                                                                  (RHON ) RHONE-POULENC BIOCH
                                                                                                                                                                                                                                                                                                                                                               Pseudomonas denitrificans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM FLC.
Browne MJ, Clinkenbeard HE, Creas
Livi GP, Southan CD;
WPI; 98-161101/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-OCT-1998 (first entry)
Homo sapiens PSP1-3 consensus sequence.
PS-1; presenilin; presenilin-1; PSP1-3; Alzheimer's disease; serine protease; neurodegeneration; predisposition; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VLPALPAPPVCDSQNECVGWLGVAYSAVVDVIRAAAHEGVYIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60; DB Pred. No. 31; 8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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RESULT W56774 ID W50

13

W56774 standard; Protein; 377 AA.

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Search completed: June 23, 2000, 10:03:38 Job time: 3366 sec
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12-AUG-1996; US-032875.

13-DEC-1996; US-032875.

13-DEC-1996; US-023436.

14-AUG-1996; US-023436.

15-COTT-1996; US-023436.

15-COTT-1996; US-023436.

16-SEP-1996; US-023436.

17-COTT-1996; US-023436.

18-COTT-1996; US-023436.

18-COTT-1996; US-023436.

19-COTT-1996; US-023436.

10-COTT-1996; US-023436.

10-COTT-1996; US-023436.

11-MAR-1998.

11-MAR-1998.

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12-COTT-1996; US-032436.

13-COTT-1996; US-032436.

14-MAR-1998.

14-MAR-1998.

15-COTT-1996; US-032436.

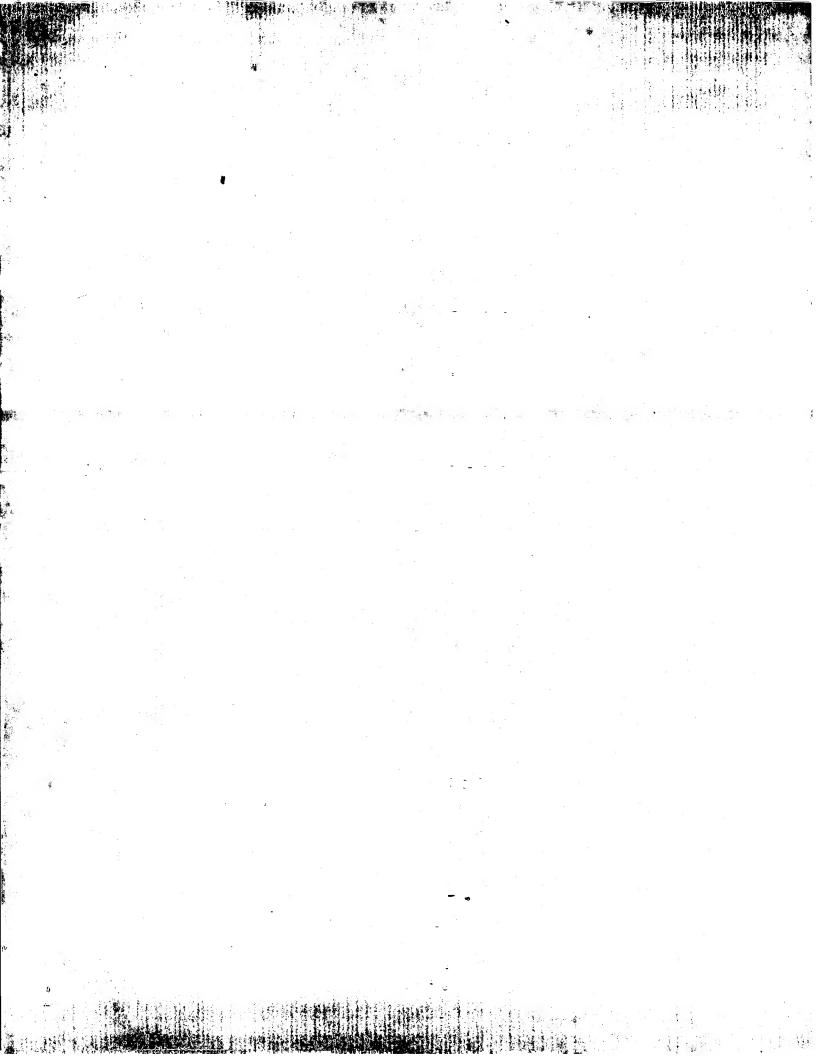
15-COTT-1996; US-032436.

16-COTT-1996; US-032436.

17-COTT-1996; US-032436.

18-COTT-1996; US-032436.

18-COTT-
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Best Local Similarity 32.6%;
Matches 14; Conservative
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Matches 17; Conservative
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PS-1; presenilin; presenilin-1; PSP1-4; Alzheimer's disease; serine protease; neurodegeneration; predisposition; diagnosis.
EP-828003-A2.
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2; Mismatches
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Total number of hits satisfying chosen parameters:
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                                                                                                                                     Matches
                                                                                                                                                           Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY_AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US, FILING DATE: June 14, 1 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth,
STREET: 805 Fifteenth
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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STREET: 805 Fifte
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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                              284 LPATIICEPISECFVASLIIGW--
                                                                                                                                                                                                                                                                                                                          LENGTH: 394 amino acids TYPE: amino acid STRANDEDNESS: single
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Post-processing: Minimum Match 0% Listing first 45

Issued\_Patents\_AA: \*

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Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.

Title:

US-09-214-478-4 621

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Patent No. 5885808
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-496-944-2
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APPLICANT: Law, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: (
NFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTECS:
LENGTH: 2763 amino acids
TYPE: amino acid
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                                                                      CORRESPONDENCE ADDRESS:
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NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 YNYYTERSKRRDRRRRSVCHARTWF-
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New York
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                                                                                                                                          Spooner, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Law, Marcus D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                                               9.9%;
                                                                                                        Compounds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monocotyledonous Plant
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                                                 Goldberg
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                                                                                                                                                                                                                                                                                                                                                            Score 61.5; DB 3;
Pred. No. 1.3e+02;
9; Mismatches 17
                                                                                                      target cells
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                                                                                                                                                                                                                                                                                                                                                                                                Length 2763;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 23; Conserv
                      MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,441B
FILING DATE: 18-DEC-197
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:151
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Romano, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 GVAYSAV-VDVIRAAAHEGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 GYTFSAYWIEWVRQAPGKGLEWVGEILPGSNNSRYNE-KFKGRVTVTRDTSTNTAYMELS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
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FILING DATE: 07/05/95
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10. 602301
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                                                                                                                                                                                                                                                                                                                                         Houston
Texas
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                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Walters, Frederick S. Slatin, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brussock, Susan M
Malvar, Thomas M.
Bryson, James W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Von Tersch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kulesza, Caroline A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English, Leigh H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --DTAVYYCARSYDFAWFAYWGQGTLVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78:
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Pred. No.
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                                                                                                                                                                                                              Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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Best Local Similarity
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/08/483,101
FILING DATE: U7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-483-101-14
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NFORMATION FOR SEQ
                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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488 MGWSGCYESYSASLSIPVKGWNSTLAYSNTY--STSVYRYDAVSEYVPYYYYKGRTKR 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 SVCHARTWFCFRKYDY-----VRRSIWHDTTINTISVVS 109
                           19 VGWLGV--AYSAVVDV-----IRAAAHEGVYIEPEARGRLDALREWIYYNYYTERSKR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 NECVGWLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIYYNYYTERSKRRDRRRR 75
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                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                          NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              ASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Conservative
                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649 amino acids
                                                                                                                                                                                                                                           890 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Froehlich, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caron, Judy
                                                                                                                                                                                             unknown
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                                                                                                                                                                                                                                                                                                                                                           33878
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                                                                                                                                                                                                                                                                                                                                              6-95
                                                                            Score 58.5;
Pred. No. 71;
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Pred. No. 41;
                                                           M1smatches
                                                                                            DB 2;
                                                             21;
                                                                                          Length 890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                    SENERAL INFORMATION:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE Townsend and Townsend and Crew LLP
ADDRESSEE: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/U8/800/....
FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: EP 95307332.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
SOFTWARE: MS WORD, WINDOWS 95, V.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                       ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                     125 -- WGQGTTVTVS 134
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STREET: 1100 New York Avenue, N.W.
STREET: 9th Floor, East Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                I: Poeschla, Eric
INVENTION: Isolation of No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                       pplication US/08659251
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VAN DER LOGT, Cornelis Paul Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                             Talbott, Randy
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                                                                                                                                             Wong-Staal, Flossie
                                                                                                                                                                  Kraus, Guenter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       October
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.2%;
25.0%;
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PCT/EP/96/03605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                          5883081el HIV-2 Proviruses
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PCT-US96-11445-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,
FILING DATE: 26-UU-1995
ATTORNEY/AGENT INFORMATION:
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                    STREET: 201
CITY: LOS Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 VCDSQNECVGWLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREW-----IYYNYYTE 65
                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: !
                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CORRENT APPLICATION DATA:
                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95
                                                                       APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein LOCATION: 1.215
OTHER INFORMATION:
                                                                                                                                                                                                                                   ZIP: 90012-2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 R--SKRRDRRRRSVCHARTWFCFRKYDYVRRSIWHDTTINTISVVSAH 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 VCYVPHHKVGWAWWTCSRVIFPLQGNSH----LEIQAYWNLTPEKGWLSSYAVRITWYTE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
               NAME: Berliner, Robert REGISTRATION NUMBER: 2
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TOPOLOGY: 11
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                           201 N. Figueroa Street, 5th Floor
                                                                                                                                                                                                                                                                                                                                                                              The Regents of the University of California VENTION: Isolation of Novel HIV-2 Proviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                           Robbins, Berliner & Carson
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24.1%;
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5555-399C1
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; MOLECULE TYPE: US-08-860-174A-12
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US-08-860-174A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 9//-10
INFORMATION FOR SEQ ID NO:
                                                                                    FILING DATE: August 14
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD, WINDOWS 95, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                            PRIOR APPLICATION DATA: EP 95307332.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 977-1001
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                                   TOPOLOGY:
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                                                                                                                                                                                                               APPLICATION NUMBER: US/08/860,174A FILING DATE: June 16, 1997
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                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UNITED STATES
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1100 New York Avenue, N.W.
9th Floor, East Tower
                                                                   274 amino acids
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                                                                                                                     October 16, 1995
MHER: PCT/EP/96/03605
August 14, 1996
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er. 4.0
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Best Local Similarity 25.0
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TRESULT 11
US-08-596-405-4
; Sequence 4, Application US/08596405
; Patent No. 5858706
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Best Local Similarity
Matches 23; Conserv
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TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,014A
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LENGTH: 1019 amino aci
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MEDIUM TYPE: Floppy disk
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                                                                                                                                       80 ARTWECERKYDYVRRSI------WHDTTTNTISVVS 109
                                                                                                                                                                                                    21 WLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIYYNYY-TERSKRRDRRRRSVCH 79
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                                                                                                      ARSF----RFDYVRSSTAGKSGCPDGWFEVDENCVYVTS 452
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8110 Gatehouse Road, Suite 500 East
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llarity 23.2%;
Conservative 1
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); Mismatches
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Pred. No. 1.
                                                                                                                                                                                                                                              Mismatches
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1.3e+02;
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Best Local Similarity 23.3
Matches 23; Conservative
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APPLICANT: Ding,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
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ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                    418 ARSF----RFDYVRSSTAGKSGCPDGWFEVDENCVYVTS 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 WGTAIYHELSSYCRAAIHAGKL--PNSGGAVHVVNNGPYSDFLGSDLNGIKSEELKSL-- 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Murphy, Jr., Gerald M REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                         TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                     80 ARTWFCFRKYDYVRRSI------WHDTTTNTISVVS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 WLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIYYNYY-TERSKRRDRRRRSVCH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                     COUNTRY: U
ZIP: 22042
                                                                                  STREET: 8110 Garen
                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22042
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                                                                                                                                                                                                                                                                                            Application US/08877620
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                                                                      Virginia
                                                                                                      E: Birch, Stewart,
8110 Gatehouse Roa
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                                                      USA
                                                                                                                                                                                                                                        Ding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                            Jeak Ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Cloned Factor C cDNA of the Singapore Horseshoe Crab, Carcinoscorpius rotundicauda and Purification of Factor C Proenzyme
                                                                                                                                                                       The Cloned Factor C cDNA of the Singapore Horseshoe Crab, Carcinoscorpius rotundicauda and Purification of Factor C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/596,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57; 1
Pred. No. 1
                                                                                                        Kolasch & Birch
d, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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US-08-471-119A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
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tent No. 5827706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFORMATION FOR SEQ ID NO: 4:
NAME: Kassenoff, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                     STREET: 57 .... CITY: East Hanover STATE: New Jersey
                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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LENGTH: 1019 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/596,405
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 17/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 ARSF----RFDYVRSSTAGKSGCPDGWFEVDENCVYVTS 452
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                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 07936
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                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                E OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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ING SYSTEM: PC-DOS/MS-DOS
E: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                 E: No. 5827706artis Corporation
59 Route 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schoergendorfer, Kurt
Weber, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schneider, Elisabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (703) 205-8050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclosporin Synthetase
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                                         100-8029/CONT/CONT
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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tolypocladium niveum
; STRAIN: ATCC 34921
US-08-471-119A-2
TELEFAX: (206) ...
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TYPE: amino acid
TYPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARATERISTICS:
LENGTH: 15281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                    TELEPHONE: (206) 727-3670
                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POOI, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3844 ICESVYDLGGDAKDSNDRVSWLSAARSNAVKVASLSAIDLVDIAQEAGFRVEISCARQW 3902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Aruffo, Alejandro A. ITITLE OF INVENTION: MONOCIONAL FITTLE OF INVENTION: Different ENTITLE OF INVENTION: In Diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3005 F. CITY: Seattle STATE: Washing:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/379,057 FILING DATE: 26-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 VCDS-----QNECYGWLGVAYSAVVDVIRAAAHEGVYIEPEA--RGRLDALREW 57
                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                    115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08379057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Gilliland, Lisa
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ilarity 30.5%;
Conservative
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Bajorath, Jurgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Siadak, Anthony W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bristol-Myers Squibb Company
                                                                                                                 727-3601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal Antibodies Specific For Different Epitopes of Human gp39 and Methods For Their User In Diagnosis and Therapy
                                                                                              31:
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Pred. No. 4.5e+03;
7; Mismatches 22;
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MOLECULE TYPE: FRAGMENT TYPE: S-08-379-057-31

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US-08-428-197-42
                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-08-428-197-42
                                                                                                                                                  Query Match 9.1%; Score 56.5; DB 2; Length 115; Best Local Similarity 21.5%; Pred. No. 8.6; Matches 20; Conservative 15; Mismatches 47; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.1%;
Best Local Similarity 21.5%;
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Patent No. 5891438
                                                                                                                                                                                                                                                                                                                       ENGTH: 115 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34.842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLB, STACY L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 ---DTAVYYCARHYDYDSYAMDYWGQGTLVTVS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 SVCHARTWFCFRKYDY -- VRRSIWHDTTTNTIS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 NYAMSWVRQAPGKGLEWV-ASISSGIYYADSVKGRFTISRDNAKNILYLQMNSLRAE--- 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 NECVGWLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIYYNYYTERSKRRDRRRR 75
                                    74 RRSVCHARTWFCFRKYDYVRRSIWHDTTTNTIS 106
                                                                      31 NYAMSWYRQAPGKGLEWYSGISASGDTTYYADSYRGRFAISRDNFKNTLYLQMNSLRAE- 90
                                                                                                              16 NECVGWLGVAYSAVVDVIR--AAAHEGVYIEPEARGRLDALREWIYYNYYTERSKRRDRR 73
90 -----DIAVYYCGRGYSY---PVWGQGTTVTVS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/428,197 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 56.5; DE; Pred. No. 8.6; 14; Mismatches
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                                                                                                                                          Indels 11;
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Search completed: June 23, 2000, 10:04:38 Job time: 2843 sec

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Searched:

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Post-processing: Minimum Match 08
Listing first 45 summaries
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Maximum DB seq length: 1000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atggttcttccagctcttcc.....cggcgcactccgtacagtag 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_est1:*
em_est2:*
em_est3:*
         9b_est1: *
9b_est4: *
9b_est4: *
9b_est5: *
9b_est6: *
9b_est6: *
9b_est10: *
9b_est110: *
9b_est111: *
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9b_est120: *
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9b_est22: *
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Result
                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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gb_est34:*
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138.4
35.4
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30.8
30.8
30.6
Unpublished (1997)
On Nov 22, 1999 this sequence version replaced gi:6462296.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                         AW276836 630 bp mrNA EST 03-JAN-2000 xp66g11.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745380 3' similar to SW:E413_ADE02 P03240 PROBABLE EARLY E4 13 KD PROTEIN.
                           Tumor Gene Index
                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                              Eutheria; Primates;
1 (bases 1 to 630)
                                                                  Homo sapiens
                                                                                             mRNA sequence.
AW276836
                                                           Eukaryota;
                                                                                      AW276836.1 GI:6663866
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AQ638467 92771-12B
W82481 mf04401.r1
AI385950 mg29506.y
AA377776 EST90394
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AQ162256 mgxb0012k
AQ35183 mgxb0021k
AQ35183 mgxb0021h
AQ891726 HS_3100_B
AW107119 um19a01.y
AI195796 u150910.x
AW412524 uq42a01.x
AW412524 uq42a01.x
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AQ841382 T136655b
AQ841373 T136636b
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AW006018 wz91g08.x
AW163374 au94d10.y
AQ944247 Sheared D
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1290263 vc90g08.

1784945 uj22a03.

1195511 ui50g10.

1217816 mu98g09.
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                                                                        AW265066 426 bp mrna EST 28-DEC-1999' xq60g03.x1 NCI_CGAP_Co22 Homo sapiens cDNA clone IMAGE:2755060 3/ similar to SW:E411_ADE02 P03241 PROBABLE EARLY E4 11 KD PROTEIN.
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Tissue Procurement: Andrew Berchuck M.D., John Gillespie
Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequenci
Clone distribution: NCI-CGAP clone distribution informat
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                               mRNA sequence.
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134 c 173 g 168 t 1 others
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/db_xref="taxon:9606"
/clone="IMAGE:2745380"
/clone_lib="NCI_CGAP_Ov39"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="papillary serous ovarian metastasis"
/lab_host="DH10B"
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GI:6641882
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98.1%;
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Pred. No. 1.5e
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.5e-85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGTTCTTCCAGCTCTTCCCGCTCCCCGTGTGTGACTCGCAGAACGAATGTGTAGGT 345
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Eutheria; Primates;
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Seq primer: -40UP from Glbco
High quality sequence stop: 425.
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Possible reversed clone: similarity on wrong strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                    W18889 303 bp mRNA EST 1(
mc04g02.rl Soares mouse p3NMF19.5 Mus musculus cDNA
IMAGE:337970 5' similar to SW:RB14_RAT p35287 RAS-RE
RAB-14. [1] ;, mRNA sequence.
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 303)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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EST.
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WashU-HHMI Mouse EST Project
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/db_xref="taxon:9606"
/clone="IMAGE:2755060"
/clone_lib="NCI_CGAP_Co22"
/tissue_type="colonic adenocarcinoma"
/lab_host="DHIOB"
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Pred. No. 1.7e-33;
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On May 9, 1995 this sequence version repla
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                AA656067 345 bp mxwa vs49hll.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone vs49hll.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:114969 5' similar to SW:RB14_RAT p35287 RAS-RELATED PROTEIN
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This clone is available royalty-free through LLNL; contact the
TMACE Consortium (info@image.llnl.gov) for further information.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Muridae; Mus.

1 (bases 1 to 345)
1 (bases 1 to 345)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Fax: 314 286 1810
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/clone="IMAGE:337970"
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/db_xref="taxon:10090"
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            Eukaryota; merman, Sciurognatur, ....
Eutheria; Rodentia; Sciurognatur, ....
1 (bases 1 to 348)
1 (bases 1 to 348)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubu Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Geisel,S., Kucaba,T., Lacy,M., Tan,F., Underwood,K., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Schellenberg,K., Steptoe,M., Soares,B., Wilson,R. and
          Theising, B., Wylie, T., Lennon, G. Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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AA562033
AA562033.1 GI:2333498
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V125e09.r1 Stratagene mouse Tcell 937311 Mus musculus
IMAGE:973288 5' similar to SW:RB14_RAT p35287 RAS-REL
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                                                                                                                                                                                     house mouse.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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The WashU-HHMI Mouse EST Project
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primer: -28m13 rev1 ET from Amersham
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on sep 12, 1996 this sequence version repl
Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                   1 (bases 1 to 389)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AA509726 389 bp mRNA EST vg20106.rl Soares mouse NDMH Mus musculus cDN 5' similar to SW:RB14_RAT P35287 RAS-RELATED
                                                                                                            The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                             Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                               house mouse
                                                                                                                                                                                                                                                                                                                                                                                       AA509726.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -28m13 rev1 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Nov 29,
Contact: Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:973288"
/clone_lib="Stratagene mouse Tcell
/tissue_type="Tcell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                       GI:2247580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.4; DB 35;
Pred. No. 0.65;
0; Mismatches 71;
                                                                                   replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA clone IMAGE:8619 PROTEIN RAB-14. ;,
                                                                                                                                                                                                                                                                             Murinae;
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                                                                                                                                                                                                                                                                                                 Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMAGE:861923
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2001- 75 ttattctgcggtggtggatgttatcagggcagcggcatgaaggagtttacatagaacc 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDS. 213 TCANACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGGTTACACGGAGCT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
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AUTHORS
                                                                                                                                                                                                                                                SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
W30475
                     COMMENT
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Best Local Similarity 52.3%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 cgaagccagggggggcgcctggatgctttgagagagtggatatactactacaactactacacaga 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 gcgatctaagcggcgagaccggagacgca 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 ACCACTTAAGCAGCTGGTTGACAGACGCA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 331.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                             W30475 453 bp mRNA EST 11-SEP-1996 mc18a09.rl Soares mouse p3NNF19.5 Mus musculus cDNA clone IMAGE:348856 5' similar to SW:RB14_RAT P35287 RAS-RELATED PROTEIN RAB-14. [1] ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800 Fax: 314 286 1810
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 453)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Unpublished (1996)
On Nov 29, 1993 this sequence version replaced g1:430269
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                            W30475.1 GI:1309206
                                                                                                                                                                                                                                                                   house mouse.
                                                                The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Mus musculus"
/strain-"C57BL/6J"
/db_xref-"taxon:10090"
/clone-"IMAGE:861923"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_mtage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares mouse
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'tissue_type="heart"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35.4; DB 34;
Pred. No. 0.68;
0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDMH.
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FEATURES
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                                                                                                                                                      REFERENCE
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Best Local
                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 TCAAACTGCAGATTTGGGATACAGCAGGGCAGGGAGCGGTTCAGAGCGGTTACACGGAGCT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 gcgatctaagcggcgagaccggagacgca 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCACTTAAGCAGCTGGTTGACAGACGCA 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78;
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Location/Qualifiers
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                                                                    Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Bukheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 477)

Marra, M., Hillier, J., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Testerrer.
                                                                                                                                                                                                                                                                                                       AA041778 477 bp mRNA EST 03-SEP-1996 mJ02g10.r1 Soares mouse embryo MbME13.5 14.5 Mus musculus cDNA clone IMAGE:474978 5' similar to SW:RB14_RAT P35287 RAS-RELATED PROTEIN RAB-14. [1]; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.3%;
Similarity 52.3%;
  Unpublished (1996)
On Jun 18, 1996 th
                                      Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                       AA041778.1 GI:1520067
                                                                                                                                                                                                                                 house mouse.
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a 89 c 100 g 109 t
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/clone 14b="r-
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    sequence version replaced g1:1366624
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AUTHORS
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                                                                                                       ORGANÍSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 ttattetgeggtggtggatgttateagggeageggegeatgaaggaggtttacatagaaec 134
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                                                                                                                                                                                                                                                                                                                                                                                                  371 ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
           Geisel,S.,
                                                                                                                                                                                             W82078 479 bp mRNA EST 12-SEP-1996 me96907.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:403452 5' similar to SW:RB14_RAT P35287 RAS-RELATED
         Marra, M., Hillier, L., Geisel, S., Kucaba, T.,
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 479)
                                                                                                   Mus musculus
                                                                                                                                                                            PROTEIN RAB-14. [1] ;, mRNA sequence. W82078
                                                                                                                                                        W82078.1 GI:1539549
                                                                                                                    ouse mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashIn-HHMI Mouse EST Project
WashIngton University School of Medicinep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone is available royalty-free through LLNL; contact the Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.3], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ. from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:474978"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.4; DB Pred. No. 0.74; 0; Mismatches
     Lacy, M., Le, M., Martin, J.,
                        Allen, M.,
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                      Bowles, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71;
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     Dietrich, N., Dut
in, J., Morris, M.,
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                                                            Mus
                                                                           Mammalia;
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                    Dubuque, T,,
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house mouse
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ORIGIN

REFERENCE

KEYWORDS VERSION ACCESSION RESULT W82078

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208 ACCACTTAAGCAGCTGGTTGACAGACGCA
                                                                                                                                                                                                           195 gcgatctaagcggcgagaccggagacgca 223
                                                                                                                                                                                                                                                                                                                                                75 ttattctgcggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacc 134
                                                                                                                                                                                                                                             ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA
                                                                                                                                                                                                                                                                     ogaagocaggggggcgcctggatgctttgagagagtggatatactacaactactactacacaga 194
                                                                                                                                                                                                                                                                                                                  TCAAACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGTTACACGGAGCT 147
AA874208
AA874208.1
                                          vx03g04.rl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1263414 5' similar to SW:RB14_RAT p35287 RAS-RELATED PROTEIN
                                       RAB-14.
                                                                                         AA874208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393029.
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer: -28M13 rev2 from Amersham
h quality sequence stop: 449.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares mouse embryo NbME13.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref="taxon:10090"
'clone="IMAGE:403452"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                         Score 35.4; DB Pred. No. 0.74; 0; Mismatches
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                                                                                     mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 479;
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                                                                                                                     RESULT 11
AI785404/c
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Best Local
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                                                                                                                                                                                                                                                                                         158
                                                                                                                                                                                                                                                                                                                                       195 gcgatctaagcggcgagaccggagacgca 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                98 ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 ttattctgcggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacc 134
                                                                                                                                                                                                                                                                                         ACCACTTAAGCAGCTGGTTGACAGACGCA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGTTACACGGAGCT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marra M., Hiller L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

Waterston, R.

The WashU-HBMI Mouse EST Project
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On Apr 18, 1995 this sequence version replaced g1:775526.
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78;
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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AI785404 513 bp mRNA EST 02-JUL-1999 uj41e10.x1 Sugano mouse kidney mkia Mus musculus cDNA cione IMAGE:1922538 3' similar to SW:RB14_RAT P35287 RAS-RELATED PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH108"
/lab_host="DH108"
/lab_nost="DH108"
/lab_nost="D
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1263414"
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Thymus"
/dev_stage="4 weeks"
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                                                                                                                                             135 cgaagccaggggggcgcctggatgctttgagagagtggatatactactactactactactacacaga 194
  239
                                                                                                    299 ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA 240
                                                                                                                                                                                                                                               75 ttattctgcggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacc 134
                                                                                                                                                                                                                                                                                                                                      Local
                                           gcgatctaagcggcgagaccggagacgca 223
ACCACTTAAGCAGCTGGTTGACAGACGCA 211
                                                                                                                                                                                                                                                                                                     10.3%;
1 Similarity 52.3%;
78; Conservation
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On Jun 22, 1998 this sequence version replaced gi:3247490.
On Jun 22, 1998 this sequence version replaced gi:3247490.
Contact: Marra M.WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
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AI785404.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: custom primer used High quality sequence stop: 451.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
MGI:978830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-Forgan: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTOTGTG); Site_2: DraIII (CACCANGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."

40 a 122 c 86 g 165 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:1922538"
/clone_lib="Sugano mouse kidney mkia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
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/lab_host="DH10B"
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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                                                                                                                               512
                                                                                                                                                                                                                                                              452 ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA 511
                                                                                                                                                                     195 gcgatctaagcggcgagaccggagacgca 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 ttattctgcggtggtggatgttatcagggcagcagcaggagcatgaaggagtttacatagaacc 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                           ACCACTTAAGCAGCTGGTTGACAGACGCA 540
                                                                                                                                                                                                                                                                                                                                       cgaagccaggggggcgcctggatgctttgagagagtggatatactacaactactacacaga 194
                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGTTACACGGAGCT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.3%;
1 Similarity 52.3%;
78; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukharyota; Medentia; Sciurognathi; Muridae; Murinae; Mus.

17' (bases 1 to 543)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wile, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
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On Sep 12, 1996 this sequence version replaced gi:14071
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Barkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Possible reversed clone: similarity on wrong strand Seq primer: -26ml3 rev1 ET from Amersham High quality sequence stop: 369.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL40104 543 bp mRNA EST 11-FEB-1997 mg93a05.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:586256 5' Similar to SW:RB14_RAT P35287 RAS-RELATED PROTEIN PAR-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA140104
AA140104.1 GI:1702468
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="heart"
/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="Solr (kanamyoin resistant)"
/lab_host="Solr (kanamyoin resistant)"
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/note="Organ; heart; Vector: pBluescript SK-; Site_1:
/note="Organ; heart; Vector: pBluescript SK-; Site_1:
/note="Organ; heart; Vector: permer:
/note="Organ; heart; Vector: primer:
/note="Organ; heart; Vector: primer: Average insert size: 1.0 kb; Un1-ZAP xx Vector; -5'
/note="Organ; heart; Vector: primer: Average insert size: 1.0 kb; Un1-ZAP xx Vector; -5'
/note="Organ; heart; Vector: primer: Average insert size: 1.0 kb; Un1-ZAP xx Vector; -5'
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/note="Organ; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; heart; hear
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/strain="NIH/Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:586256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Stratagene mouse heart (#937316)"
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Pred. No. 0.79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 543;
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LOCUS
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VERSION
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Best Local S
Matches 78
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                                                                         ACCACTTAAGCAGCTGGTTGACAGACGCA
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133 TCAAACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGGTTACACGGAGCT 192
195 gcgatctaagcggcgagaccggagacgca 223
                                                                                                                                                                            75 ttattctgcggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacc 134
                                                   ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAAAAGAAGTACATATA
                                                                                                 cgaagccaggggggcgcctggatgctttgagagagtggatatactacaactactacacaga 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393035.
Contact: Maria Myouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 547)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA290263 547 bp mRNA EST 14-APR-1997 vc90g08.rl Barstead MPLRB1 Mus musculus cDNA clone IMAGE:790334 5' similar to SW:RB14_RAT P35287 RAS-RELATED PROTEIN RAB-14. ;, mRNA
                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="IMAGE:790334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Barstead MPLRB1"
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                                                                                                                                                                                                                                                               10.3%;
                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                         Score 35.4; DB 31;
Pred. No. 0.79;
0; Mismatches 71;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                        Length 547;
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BASE COUNT
ORIGIN
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AUTHORS
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AI784945/c
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VERSION
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Best Local S
Matches 78
341
                                              135 cgaagccaggggggcgcctggatgctttgagagagtggatatactacaactactacacaga 194
                                                                                                        60
                                                                                                                                   ttattctgcggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacc 134
ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACCACCAGAAGAAGTACATATA 282
                                                                                                     TCAAACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGTTACACGGAGCT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Jun 22, 1998 this sequence version replaced gi:3247058. Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI784945 551 bp mRNA EST 02-JUL-1999 uj22a03.x1 Sugano mouse kidney mkia Mus musculus CDNA clone IMAGE:1920652 3' similar to SW:RB14_RAT P35287 RAS-RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 551)
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AI784945.1 GI:5332696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possible reversed clone: similarity on wrong strand Seq primer: custom primer used High quality sequence stop: 481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAB-14.
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                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                       150
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                            /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCTGTGTG); lst strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTACTGTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], dyested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCACCTCAACCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Mus musculus"
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/clone-"1MAGE:1920652"
/clone_lib-"Sugano mouse kidney mkia"
/sex-"female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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                                                                                                                                                                                                                                10.3%;
                                                                                                                                                                                                          0
                                                                                                                                                                                                        Score 35.4; DB 60;
Pred. No. 0.79;
0; Mismatches 71;
                                                                                                                                                                                                                                                            Length 551;
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Query Match Best Local S Matches 78

Similarity

10.3%;

Score 35.4; D: Pred. No. 0.8; O; Mismatches

80 띪

Indels Length

0

Gaps

Conservative

75 ttattctgcggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacc 134

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RESULT 1
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On Jan 19, 1998 this sequence version replaced g1:228694
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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u150g10.yl Sugano mouse liver mlia Mus musculus cDNA
IMAGE:1885890.5' similar to SW:RB14_RAT P35287 RAS-RE
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1 (bases 1 to 556)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Marrin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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                             Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCCACA."

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/strain="C57BL"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib-"Sugano mouse liver mlia"
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th com	528	195	468	135	408
Search completed: June 23, 2000, 09:17:14 Job time: 12882 sec	7	195 gegatetaageggegagaceggagaegea 223	ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA 527	135 cgaagccagggggcgcctggatgctttgagagagtggatatactactacaactactacacaga 194	408 TCAAACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGTTACACGGAGCT 467
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1 atgyttcttccagctcttcccggcgcactccgtacagtag 345  able: IDENTITY_NUC Gapop 10.0 , Gapext 1.0  731313  311585 seqs, 125096042 residues ' ID	38 39 3 - nucleic search, using sw model  June 23, 2000, 10:05:42; Search time 56.99 Seconds  (without alignments)  (US-09-214-478-3  1514.586 Million cell updates/sec  1 atggttcttccagctcttcccggcgcactccgtacagtag 345  able: IDENTITY_NUC Gapop 10.0 , Gapext 1.0  31585 segs, 125096042 residues  38 40 40 41 41 41 42 42 43 44 45 47 48 49 40 41 41 41 41 41 41 41 41 41 41 41 41 41
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Adenovirus E4 and part ITR research man adenovirus; inverted tar expression; late gene; cell licomplementation; gene therapy, neurodegenerative disease; ble Adenovirus Ad5.  25-UUI-196; FR-000747.  21-UNI-1995; FR-000532.  20-JAN-1995; FR-00532.  20-JAN-1995; FR-00532.  20-JAN-1995; FR-010541.  20-JAN-1995; FR-010541.  20-JAN-1995; FR-010541.  20-JAN-1995; FR-010542.  20-JAN-1995; FR-010543.  20-JAN-1995; FR-010543.  20-JAN-1995; FR-010543.  20-JAN-1995; FR-010543.  20-JAN-1995; FR-010543.  20-JAN-1995; FR-010541.  20-JAN-1996; FR-000747.	LT 1 15/c 731315 stand 731315; 16-APR-1997	N 8
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cc method of the invention. The plasmid contains an adenovirus type 5 (E4 regulatory gene and a hygromycin resistant gene. The invention cc provides adenoviral vectors having deletions of all or part of carlous gene sequences encoding adenoviral structural proteins. CC Deletions in the structural proteins would allow a reduced risk of cc wild type virus contamination and would also allow packaging of foreign CC DNA in such vectors for a variety of diagnostic and therapeutic CC applications. The adenoviral vectors having deletions in the structural cc gene regions are produced by cellular complementation of these cc adenoviral genes. Therefore, the pE4/Hygro plasmid was used as a cc complementation plasmid which was introduced into a host cell line complementation plasmid which was introduced into a host cell line complementation plasmid which was introduced into a host cell line complementation plasmid which was introduced into a host cell line complementation plasmid which was introduced into a host cell line complementation plasmid who was used as a gene delivery vector. The vectors can be used for diagnosis or cg gene therapy, e.g. for treating conditions characterised by the cc gene therapy, e.g. for treating conditions characterised by the cc. Huntington's disease, Tay-Sachs disease, or sickle cell disease), or cc production of biologically active proteins.

SQ. Sequence 8710 BP; 2263 A; 2365 C; 2141 G; 1941 T;
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The present sequence is that of a pE4/Hygro plasmid used in the method of the invention. The plasmid contains an adenovirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete sequence of the pE4/Hygro plasmid.
Circular; adenovirus type 5; pE4/Hygro plasmid; structural protein;
complementation; E4 regulatory protein; gene therapy; HIV: tumour;
Huntington's disease; Tay-Sachs disease; sickle cell disease;
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(SCRI ) SCRIPPS RES INST.
Memerow GR, Von Seggern DJ;
WPI; 98-230709/20.
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24-SEP-1997; E05251.
25-SEP-1996; US-719806.
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V32370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      denoviral vectors - which lack DNA encoding for structural protein
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PA (NOVS) NOVARTIS AG.

PI Memerow GR, Von Seggern DJ;

PI Memerow GR, Von Seggern DJ;

PI Memerow GR, Von Seggern DJ;

PT Adenoviral vectors - which lack DNA encoding for structural protein

PT or fibre protein used particularly for gene therapy

PS Example 1; Pages 131-145; 170pp; English.

CC The present sequence is that of a pE4/Fiber plasmid used in the

CC method of the invention. The plasmid contains an adenovirus type 5 (AD5)

CC fiber gene controlled by a CMV promater, an AD5 E4 gene and an adenovirus

CC type 2 (AD2) tripartite leader sequence upstream of the fiber gene. The

CC various gene sequences encoding adenoviral structural proteins and/or

CC various gene sequences encoding adenoviral structural proteins and/or

CC early region proteins. Deletions in these proteins would allow a

CC cearly region proteins. Deletions in these proteins would also allow

CC packaging of foreign DNA in such vectors for a variety of diagnostic and

The adenoviral vectors having deletions in
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Best Local
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24-SEP-1997; E05251.
25-SEP-1996; US-719806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete sequence of the pE4/Fiber plasmid. Circular; adenovirus type 5; pE4/Fiber plasmid; stru complementation; fiber protein; gene therapy; HIV; tearly gene; Huntington's disease; Tay-Sachs disease;
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sickle cell
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therapeutic applications. The active structural and/or early gene
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345; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "AD5 leader sequence" 4372. .6124
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4051. .4366
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The adenoviral vectors having deletions in y gene regions are produced by cellular
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Pred. No. 8.2e-105;
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AD5;
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Best Local Similarity
Matches 345; Conserv
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and durable transgene expression

Example 2; Fig 10A-H; 74pp; English.

This is the DNA sequence of the recombinant adenovirus

H5.020TKneo-int. It was obtained by co-transfecting HEK293 (ATCC CRL1573) cells with linearised plasmid padneo-int (see T60555) and Ad5d17001. It was used as a control in studies of the retrotransposition and integration of cis- and trans-acting recombinant adenoviruses (see T60557 and T60558) into host cells. Claimed novel recombinant replication defective viruses (A) comprise: (a) DNA of, or corresponding to, at least part of the viral genome, able to infect a mammalian cell; and (b) a first
                                                                                                                                                                                                                                                                                                                                                                                   01-MAY 1997.
01-MAY 1997.
24-OCT-1996; U17176.
27-OCT-1995; US-005942.
27-OCT-1995; US-005942.
(UYPE-) UNIV PENUSYLVANIA.
Relley WM, Wilson JM;
WPI; 97-259031/23.
MPI;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1998 (first entry)
Recombinant adenovirus H5.020Tkneo-int.
Adenovirus H5.020Tkneo-int; plasmid pAdmLVneo-int; Ad5; Mo-MLV;
retrovirus; retrotransposition; transposition; transgene;
gene therapy; vector; neomycin resistance; neo gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1531
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T60559;
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Pred. No. 8.9e-105;
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Best Local (
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Adenoviral vector plasmid pBHG11.
Adenovirus 5; Ad5; vector; gene therapy;
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                                                                                          8773.
                                                                                                                                                              Location/Qualifiers'
8772. .9385
                                                                                        100.0%;
"region deleted in plasmid paxBdelpoldelpTPVARNA+tl3 and pBHG11delpolydelpTPVARNA+t13 .11134
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Pred. No. 1.4e-104;
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                 (Claim
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misc\_feature

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FS Claim 45; Page 87-102; 139pp; English.

CC This nucleotide sequence comprises plasmid pBHG11 that consists of CC and 5 (see also V07258) from bp 188-1339 (0.5-3.7 m.u.). This deletion removes the packaging signals as well as El sequences. CC pBHG11 also contains a large deletion within the E3 region (bp CC 27865-30995, 77.5-86.2 m.u.). Mucleotide 873 of pBHG11 is equivalent to nucleotide 7269 of Ad5. The large E3 deletion CC provides a large cloning capacity to Ad vectors based on pBHG11. CC Recombinant plasmids pdelpol and pBHG11delpol (deleted for E1 and CC polymerase functions), and pAXBdelpoldelpTVARNA+t13 and CC polymerase functions), and pAXBdelpoldelpTVARNA+t13 and CC preterminal protein functions), are specifically claimed. The CC invention provides improved adenoviral vectors and packaging CC within the E3D region of the adenoviral genome (see also V07261). CC These E2D-deleted virus are used in conjunction with novel cell (CC vittin the E3D region of the adenoviral genome (see also V07261). CC significations permit the transfer of large genes (e.g. up to CC provide improved adenoviral genome (see also V07261). These E2D-deleted for E1 viral coding regions. These CC grutted vectors permit the transfer of large genes (e.g. up to CC provide improved adenoviral genome (see also V07261). These E2D region of the E2D-deleted and gutted vectors of CC provide improved adenoviral vectors useful for a wide variety of CC gene therapy applications.

200 gene therapy applications.

201 gene to the muscle of mice. The E2D-deleted and gutted vectors of CC gene therapy applications.

202 gene therapy applications.
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Best Local Similarity

Matches 345; Conserv
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Amalfitano A, Chamberlain JS,
Hauser MA, Kumar-Singhr;
WPI; 98-261485/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New adenoviral recombinant plasmid(s) for expression of large foreign DNA f. therapy of genetic disease(s)
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23-OCT-1996;
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                                                                            cgcacctggtttttgcttcaggaaatatgactacgtccggcgttccatttggcatgacact
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                                                       CGCACCTGGTTTTGCTTCAGGAAATATGACTACGTCCGGCGTTCCATTTGGCATGACACT
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/*tag=
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100.0%; Pred. No. 1.4e-104;
tive 0; Mismatches 0;
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pAXBdelpoldelpTPVARNA+t13 and
pBHG11delpolydelpTPVARNA+t13 (Claim 53)"
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"region deleted in plasmid phHG11delpTP (Claim 51)"
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    comprise sequences provided
ragments, used for, e.g. gene

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Best Local
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Blazing MA, George SE;
WPI; 99-204005/17.
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Recombinant adenovirus Ad:Pac-beta-Gal; replication deficient adenovirus;
Recombinant adenovirus Ad:Pac-beta-Gal; replication deficient adenovirus;
Ela region; E3 region; gene therapy; nitric oxide synthetase; NOS;
cystic fibrosis chloride channel; LDL receptor; erythropoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atherosclerotic arteries.
74787 RP: 7923
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X15627 standard;
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09-MAR-1999.
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07-мау-1999
                                                                                                                                                                                                                                                                                                                             121
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17-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 100.0%;
Local Similarity 100.0%;
tes 345; Conservative 0
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                                                                                                                                                                   aactactacacagagcgatctaagcggcgagaccggagacgcagatctgtttgtcacgcc
                                                                                                                                                                                                                                                                                                gtttacatagaacccgaagccaggggggcgcctggatgctttgagagagtgggatatactac
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         CGCACCTGGTTTTGCTTCAGGAAATATGACTACGTCCGGCGTTCCATTTTGGCATGACACT
                                             GTTTACATAGAACCCGAAGCCAGGGGGGCGCCTGGATGCTTTGAGAGAGTGGATATACTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 345; DB 1;
Pred. No. 1.4e-104;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9880 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9421 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 34382;
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32244
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301 acgaccascacgatctcggttgtctcggcgcactccgtacagtag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Principle of the presence of transposase, providing stable principle and durable transgene expression

Example 2; Fig 8A-1; 74pp; English.

CThis is the DNA sequence of the cis-acting recombinant adenovirus CC His-0207kneo-int(LTR). It was obtained by co-transfecting HEX293 CC (ATCC CRL1573) cells with linearised plasmid pAdMLVneo-int (198e 760554) and Ad5617001. A trans-acting adenovirus (see CC F00558) was also produced, and retrottransposition and integration cc viruses. Claimed novel recombinant replication defective viruses (A) comprise: (A) DNA of, or corresponding to, at least part of the CC viruses. Claimed novel recombinant replication defective viruses (C) the cis-acting terminal repeat sequences of a transposon, and ESI CC expression sequence (ESI) comprising a human gene (I) linked to regulatory sequences for expression, with the cassette flanked by the cis-acting terminal repeat sequences of a transposon, and ESI CC express (I) and transfer it to the cellular chromatin vivo or in CC express (I) and transfer it to the cellular chromatin vivo or in CC transposase gene (II) plus regulatory sequences, flanked by DNA of (A); (A) can infect a mammalian cell; and (2) mammalian cells which stably express (I) integrated into its chromatin, produced by infection with (A). (A) are also used to express transposase (I) integrated into its chromatin, produced by infection with (A). (A) are also used to prepare (C claimed), e.g. in somatic gene therapy of genetic defects or deficiencies such as cystic fibrosis. (A) are also used to prepare (C claimed) integrated, it provides longer lasting expression than genes culturoduced with conventional adenoviral vectors and the need for cepatated administration is avoided. The transgene is inherited by the coll control of the viral component is gradually degraded by the cccl.
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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27-OCT-1995; US-005942.
(UTPE-) UNIV PENNSTLVANIA.
Kelley www. w11son JM;
WPI; 97-259031/23.
                                                                                                      33407
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                                                                                            tggctgggtgtggcttattctgcggtggtggatgttatcagggcagcggcatgaagga 120
                                                                                                                                                                                                                                                                                                   al Similarity
345; Conserv
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                                                                                                                                                                                                                                                                                         100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7810 A;
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                                                                                                                                                                                                                                                                                         Score 345; DB 1; Pred. No. 1.4e-104; No. 1.4e-104; No. 1:4e-104; No. 1:4
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181 aactactacacagagcgatctaagcggcgagacccggagacgcagatctgtttgtcacgcc

55 A 55

121

61

34282 TGGCTGGGTGTGGCTTATTCTGCGGTGGTGGATGTTATCAGGGCAGCGGCGCGCATGAAGGA

tggctgggtgtggcttattctgcggtggtggatgttatcagggcagcggcgcatgaagga 120

GTTTACATAGAACCCGAAGCCAGGGGGGCGCCTGGATGCTTTGAGAGAGTGGATATACTAC

34163

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                                                                                                                                         New adenoviral recombinant plasmid(s) - comprise sequences provided for expression of large foreign DNA fragments, used for, e.g. gene therapy of genetic disease(s)

Disclosure; Page 69-86; 139pp; English.

This nucleotide sequence comprises the adenovirus 5 (Ad5) genome. The invention provides improved adenoviral vectors and packaging cell lines. One type of improved vector comprises deletions within the E2b region of the adenoviral genome (see also V07261). These E2b-deleted virus are used in conjunction with novel cell lines that constitutively express E2b gene products. The invention also provides vectors deleted for all viral coding regions. These (suptous provides vectors deleted for all viral coding regions. These (gutted vectors permit the transfer of large genes (e.g. up to the muscle of mice. The E2b-deleted and gutted vectors gene to the muscle of mice. The E2b-deleted and gutted vectors gene to the muscle of mice. The E2b-deleted and gutted vectors gene therapy applications.

Sequence 35935 BP; 8367 A; 10074 C; 9760 G; 7734 T;
                                                                 Query Match
Best Local S
Matches 345
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23-OCT-1997; U19541.
23-OCT-1996; US-735609.
(UNMI ) UNIV MICHIGAN.
Amalfitano A, Chamberlain J.
Hauser MA, Kumar-Singhr;
WPI; 98-261485/23.
33227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adenovirus 5 genome.
Adenovirus 5; Ad5; vector; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mastadenovirus 5.
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                                                                 Local Similarity
mes 345; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA; 35935
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS, Hartigan-OConnor DJ
                                                                 0
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                                                               Score 345; DB 1;
Pred. No. 1.5e-104;
; Mismatches 0;
                                                                                              Length 35935;
                                                                 Indels
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S
                                                                                                                                       Fr and durable transgene expression

Example 2; Fig 9A-1; 74pp; English.

CC This is the DNA sequence of the trans-acting recombinant adenovirus

CC H5.020CMygag-pol. It was obtained by co-transfecting HEK293

CC (ANCC CRL1573) cells with linearised plasmid pAdCMygag-pol (see

CC T60555) and Ad5d17001. A cis-acting adenovirus (see T60557) was

CC calls was demonstrated in HeLa cells infected, with both yiruses.

CC claimed novel recombinant replication and integration into host

CC comprise: (a) DNA of, or corresponding to at least part of the

CC viral genome, able to infect a mammalian cell; and (b) a first

CC viral genome, able to infect a mammalian cell; and (b) a first

CC viral genome, able to infect a mammalian cell; and (b) a first

CC viral genome, able to infect a mammalian cell; and (b) a first

CC viral genome, able to infect a mammalian cell; and (b) a first

CC viral genome, able to infect a mammalian cell; and (b) a first

CC viral genome, able to infect a mammalian cell; and (b) a first

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CC viral genome, and transfer it to the cellular chromatin in vivo or in

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CC viral genome, and transfer it to the cellular chromatin in vivo or in

CC viral genome, and transfer it to the cellular chromatin in vivo or in

CC viral genome, and transfer it to the cellular chromatin in vivo or in

CC viral genome, and transfer it to the cellular chromatin in vivo or in

CC viral genome (II) plus regulatory sequences, flanked by

CC and a second expression sequence (ES2) containing a las above

CC and a second expression sequence (ES2) containing a las above

CC and able to express transposase in mammalian cells; and (2)

CC and able to express transposase
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adenovirus H5.020CMVgag-pol.
Adenovirus H5.020CMVgag-pol; plasmid pAdMIVneo-int; Ad5;
retrovirus; retrotransposition; transposition; transgene;
gene therapy; vector; ss.
Chimeric - Mastadenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 34042 ACGACCAACACGATCTCGGTTGTTCTCGGCGCACTCCGTACAGTAG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Mastadenovirus serotype 5.
Chimeric - Moloney murine leukaemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant replication defective virus - inserts transgene into host cell chromatin in the presence of transposase, providing stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-1996; U17176.
27-OCT-1995; US-005942.
(UYPE-) UNIV PENNSYLVANIA.
Kelley WM, Wilson JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9715679-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T60558 standard; DNA; 36538
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Local Similarity
les 345; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97-259031/23.
                                                                                                              retrovirus. - 36538 BP;
                       100.0%;
                                                                                                              8621 A;
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                       Score 345; DB 1;
Pred. No. 1.5e-104;
    M1smatches
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Example 10; Fig 28A, XX; 126pp; English.

CC This is the nucleotide sequence of vector 231-10, a human cadenovirus serotype 5 (Ad5) vector. 231-10 lacks the E1A, E1B cc and E3 transcription units. The deleted E1A and E1B regions are creplaced with an expression cassette wherein all the E3 proteins care expressed from the human cytomegalovirus (CMV) promoter. The CC are expression cassette contains the E3 genes from virus pm734.1, CC a derivative of virus rec700, which is an Ad5-Ad2-Ad recombinant ct that has the Ad2 version of the E3 genes for the 12.5K, 6.7K, CT that has the Ad2 version of the E3 genes for the 12.5K, 6.7K, CT that has the Ad2 version of the E3 genes for the 12.5K, 6.7K, CT that has the Ad2 version of the E3 genes for the 2.5K, 6.7K, CT that has the Ad2 version of the E3 genes for the 2.5K, 6.7K, CT that has the Ad2 version of the E3 genes for the E3 genes cc for the RID-beta and 14.7K proteins. In addition, the vector has cc missense mutations in the adp (adenovirus death protein) gene cc that eliminate the first 2 Met codons, thereby precluding synthesis cof functional ADP. Because 231-10 lacks E1A, viral genes in the CC vector backbone are not expressed; only the E3 proteins are expressed from the CMV promoter. Thus, the vector serves as an cc expressed from the CMV promoter. Thus, the vector serves as an cc expressed from the CMV promoter. Thus, the vector serves as an cc expressing a death receptor of the tumour necrosis factor creceptor family. This involves treating the cells with a receptor internalisation and degradation (RID) protein complex containing cell can be treated by administering to the cell a polynuclectide complex. The compositions and methods are used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Mastadenovirus 5.
Chimeric - Mastadenovirus 2.
Chimeric - Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adenovirus vector 231-10 genome.
Adenovirus; vector 231-10; apoptosis; inhibitor; RID-alpha;
RID-beta; receptor internalisation and degradation; cancer;
degenerative disease; immune disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1998;
09-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9902658-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue transplant; death receptor; tumour human; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      degradation (RID) complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for inhibiting apoptosis - using receptor internalisation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 99-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                   17-AUG-1998 (first entry)
(Chimpanzee adenovirus C68 genomic sequence.
genomic sequence; virus genomic sequence.
genomic sequence; virus genomic sequence.
acquired defects; inherited defects; genetic engineering;
an vitro production; recombinant protein; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                degenerative immunodeficiency diseases, particularly to decrease leukocyte apoptosis (claimed). Immune disorders that can be treated include autoimmune disorders, ischaemic injury such as caused by myocardial infarction, stroke induced neuron death and reperfusion injury, alcohol-induced hepatitis, diseases caused by viral infection such as AIDS and fulminant hepatitis, and cancer. The methods can also be used to promote tissue transplant survival. Vector 231-10 can be used to deliver the RID complex to
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                                            complement(36193.
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10823.
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complement(10346.
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complement(23370.
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99.7%;
                                                                                                      "E2B gene"
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                                        "E4 gene"
 "L1 gene
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Pred. No. 4.9e-104;
D; Mismatches 1;
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Best Local Similarity
Matches 217; Conserv
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04-SEP-1997; U15694.

06-SEP-1996; US-024700.

(UYPE-) UNIV PENNSYLVANIA.

Farina SF, Fisher KJ, Wilson JJ

WPI; 98-193635/17.
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The sequence is that of the chimpanzee adenovirus C68. It may used in the production of a vector comprising it and a select heterologous gene operatively linked to regulatory sequences directing its expression in a heterologous cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Such recombinant adenoviruses are useful as vectors in gene therapy and genetic engineering in general, especially for the treatment of aquired or genetically inherited defects. The viruses are also useful for the in vitro production of recombinant proteins of interest.

Sequence 36519 BP; 7809 A; 10790 C; 10623 G;
         Chimpanzee adenovirus Cl genomic sequence. genomic sequence; virual genome; virus; gene therapy; acquired defects; inherited defects; genetic engineer in vitro production; recombinant protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             engineering in general
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimpanzee adenovirus vector - useful in
                                                                  17-AUG-1998
                                                                              V22140 standard;
V22140;
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17480.
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32134.
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.27439
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.21804
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Pred. No. 1e-37;
0; Mismatches 122;
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a selected
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04-SEP-1997; U15694.
06-SEP-1996; US-024700.
(UYPE-) UNIV PENNSYLVANIA.
Farina SF, Fisher KJ, Wilson J
WPI; 98-193635/17.
                                  33874
                                                                                       33934
                                                                                                                                                                                                                                                                                                   theterologous gene operatively linked to regulatory sequences directing its expression in a heterologous cell. Such recombinant adenoviruses are useful as vectors in gene therapy and genetic engineering in general, especially for the treatment of aquired or genetically inherited defects.
                                                                                                                                                                                                                                                            the treatment of aquired or genetically inherited defects. The viruses are also useful for the in vitro production of recombinant proteins of interest.

Sequence 35524 BP; 8873 A; 9142 C; 9033 G; 8
                                                                                                                                                                                                                                                                                                                                                                    engineering in general
Disclosure: Pages 51-70; 116pp; English.
The sequence is that of the chimpanzee adenovirus C1.
used in the production of a vector comprising it and a
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                                                                                                                                     aactactacacagagcgatctaagcggcgagaccggagacgcagatctgtttgtcacgcc 240
                             GTTTTCATAACAACTGAAGCCGAGGAACTTTTGACCAATCTACGGGAATGGCTGTACTTC
                                                9tttacatagaacccgaagccagggggcgcctggatgctttgagagagtggatatactac 180
                                                                                                 tggctgggtgtggcttattctgcggtggtggatgttatcagggcagcggcgcgcatgaagga 120
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omplement(10379.
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omplement(35228.
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omplement(23665.
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.22083
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.32551
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.27813
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Pred. No. 3.6e-24;
0; Mismatches 110
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                                                                                                                                    polya_signal
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Ad2/-ORF6/PGK-CFTR nucleotide sequence
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Q68003;
26-MAR-1996 (first e
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20240
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12915. .36335
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note= "Peripentonal hexon-associated protein"
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                                        "Hexon . 23983
                                                                                                                                                                                         "Precursor .19887
                                                                                                                                                                                                                                            "virion component .18708
"Virion
                                                                                             "major
.20992
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                                                                                                                                    .20193
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Hexon protein irion component II"
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                                                    associated precursor'
                                                                  protein
                                                                                                        late mRNA L2 poly-A signal (putative)"
                                                                                                                                                  core
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to major core protein"
                                                                                                                                               protein"
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Adenovirus based gene therapy vectors - esp. useful for gene Adenovirus based gene therapy vectors - esp. useful for gene Adenovirus vector named Ad2-ORF6/PGK-CFTR. This virus lacks El and in its calcaloration adenovirus vector named Ad2-ORF6/PGK-CFTR. This virus lacks El and in its calcaloration vector named Ad2-ORF6/PGK-CFTR. This virus lacks El and in its calcaloration vector named Ad2-ORF6/PGK-CFTR. This virus lacks El and in its calcaloration vector named Ad2-ORF6/PGK-CFTR, this virus lacks El and in its calcaloration vector named Ad2-ORF6/PGK-CFTR, const. The EA region of the Vactor has also been modified to fibrosis transmembrane condutance regulator (CFTR) conMa. The PGK calcalorate strength but it is long lasting and is not construct to shut off. The EA region of the vactor has also been modified in that the whole sequence has been removed and replace by ORF6, the construct comprises a full length copy of the Ad2 genome from the DNA construct comprises a full length copy of the Ad2 genome from the CC which the early region 1 genes (El genes) have been deleted and replaced by an expression cassette encoding CFTR. The expression cassette conductes the promoter for PGK and a poly-A addition signal from the CC includes the promoter for PGK and a poly-A addition signal directly construct differs and constructed the the pulmostry allocation signal directly constructed the pulmostry allocation signal directly constructed the pulmostry allocation signal directly constructed the pulmostry allocation signal directly constructed the pulmostry allocation signal directly constructed the pulmostry allocation signal directly constructed the pulmostry allocation signal directly constructed the pulmostry allocation signal directly constructed the pulmostry allocation signal directly constructed the pulmostry allocation signal directly constructed the pulmostry allocation signal directly constructed the pulmostry allocation signal directly constructed the pulmostry signal constructed the pulmostry signal constructed the
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02-DEC-1993; U11667.
03-DEC-1992; US-985478.
01-OCT-1993; US-130682.
13-OCT-1993; US-136742.
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33081.
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35013.
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32008.
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/note= "Glycosylated mem]
31707. .32012
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31051.
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1011. .5453
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/note= "Hexon assembled"
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lement (244729. .26318)
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.31530
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the gene therapy of cystic
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PT Recombinant adeno-associated virus contg. second gene which from the facilitates its conversion from single stranded to double stranded the facilitates its conversion from single stranded to double stranded for virus - enhances efficiency of ex vivo transduction into target cell for virus - enhances efficiency of ex vivo transduction into target cell for the facilitation of the mouse manmary tumour virus promoter and a growth hormone control of the mouse manmary tumour virus promoter and a growth hormone terminator sequence. The minigene is used to generate a packaging cell line expressing the 24 ORFS product which is used to rescue and package comprises at least 2 selected genes, the first gene able to express the comprises at least 2 selected genes, the first gene able to convert the single stranded virus to its double stranded gene able to convert the single stranded virus to its double stranded form upon expression. The rAAV is useful in pharmaceutical compositions for use in ex vivo and convert convert convert the target convert the target convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert convert conver
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27-AUG-1997
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                             (UYPE-) UNIV PENNSYLVANIA. Fisher KJ, Gao G, Wilson
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05-JUN-1995; US-462014.
27-OCT-1995; US-549489.
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12-DEC-1996.
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foote= "specification gives this CDS at nucleotides
1523-2408"
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/note= "mouse mammary
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Query Match
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Matches 80; Conserv

Conservative

23.2%; >--100.0%; Pr

Score 80; Pred. No.

DB 1; I 6.2e-17;

Length 3653

Mismatches

Indels

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Gaps

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DE: Second generation recombinant adenoviral vector pAV.CMVALP.GRE-ORF6.

KNY-Minigener human adenovirus type 5; open reading frame; promoter; in vivo;

KNY-Minigener human adenovirus; growth hormone; terminator; recombinant;

KNY-TPACKAGING.cell line; adeno-associated virus; ex vivo; gene therapy;

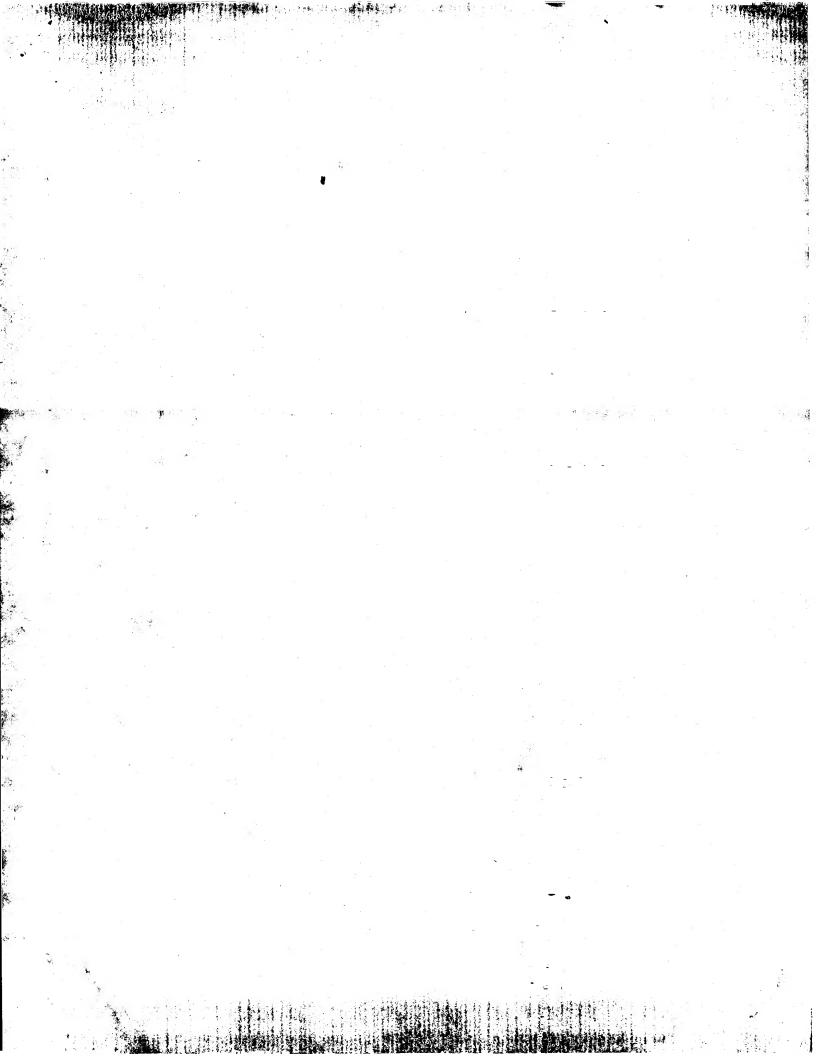
KNY-TIMETITED disease; cancer; genetic dysfunction; cystic fibrosis; ds.
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04-JUN-1996; US-462014.
05-JUN-1995; US-549149.
27-OCT-1995; US-549489.
(UYPE-) UNIV PENNSTLVANIA.
Fisher KJ, Gao G, Wilson JM;
WPI; 97-043152/04.
Recombinant adeno-associated virus contg. second gene which facilitates its conversion from single stranded to double stranded virus - enhances efficiency of ex vivo transduction into target cell Example 19; Page 108-114; 131pp; English.

This is the nucleotide sequence of a second generation of recombinant adeno-associated virus (rAAV) which contains 2 genes, the first gene able to express the gene of interest (beta-galactosidase) in the target cell; and the second gene(AdS 24 ORF6) able to convert the single stranded virus to its double stranded form upon expression. The rAAV is useful in pharmaceutical compositions for use in ex vivo and in vivo gene therapy for the treatment of inherited diseases, cancer and other genetic dysfunctions, e.g. cystic fibrosis.

See also T59271 for amouther example of a recombinant adeno-associated
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'note= "3' AAV ITR"
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note= "cytomegalovirus enhancer/promoter"
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345 3481	atttggcatga           ATTTGGCATGA	%; Score 8 0%; Pred. 0; Mism	1816 A; 21
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Search completed: June 23, 2000, 10:06:58 Job time: 3686 sec



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Sequence 4 from Patent WO9622378.
A52460
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Other publication AU 4544396 960807
Other publication FR 2729674 960726
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Dedieu,7., Latta,M., Orsini,C., Per
CELLS FOR THE PRODUCTION OF RECOMBI

Patent: WO 9622378-A 4 25-JUL-1996;
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                                                                                                        protein 5 precursor; protein IIIa; protein V; protein pVI; protein pVIII.

Buman adenovirus 5 DNA.

Human adenovirus type 5

Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

1 (bases 1 to 35935)
                                                                                                                                                                                                                   ADRCOMPGEN 35935 bp
Mastadenovirus h5 gene,
M73260 M29978
                                          The sequence of the genome of adenovirus type 5 and its with the genome of adenovirus type 2
Virology 186 (1), 280-285 (1992)
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                                                                                       Chroboczek, J., Bleber, F. and Jacrot, B.
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/db_xref="taxon:32644"
912 c 631 g 67
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Pred. No. 5.5e-97;
                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                     complete genome
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ADENOVIRUSES
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RRQPVLAPISYRRVAREGGRTLVLPTARYHPSIV"
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35937 bp

Adenovirus type 2, complete genome.

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J01927 J01928 J01929 J01930 J01931 J01932 J01933 J01934

J01935 J01936 J01937 J01938 J01939 J01940 J01941 J01942 J01943

J01935 J01936 J01946 J01947 J01948 J01949 J01950 J01951 J01952

J01944 J01945 J01946 J01947 J01948 J01949 J01950 J01951 J01952

J01953 J01954 J01955 J01956 J01957 R00086 K00394 K00395 K02367

M13004 W00007 W00008 W00009 W00001 W00012 W00013 W00014

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                                                                                                                                       alternative splicing; coat protein; protein; glycoprotein; overlapping ; repeat; unidentified reading frame;
                                                                        Human adenovirus type 2.
Human adenovirus type 2
Viruses; dsDNA viruses, no
                                                                                                                                                                                                      DNA polymerase; DNA-binding protein; RNA polymerase III;
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SFTPRQAILTLQTSSSEPRSGGIGTLQFIEEFVPSVYFNPFSGPPGHYPDQFIPNFDA
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Mismatches 0;
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              Shinagawa, M.
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                                                                                                                                                                                                                                                      Nucleotide sequence analysis of copy of adenovirus 2 fiber mRNA Cell 16 (4), 851-861 (1979), 702172/0
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Arrand, J.R. and Roberts, R. J.
The nucleotide sequences at the termini
J. Mol. Biol. 128 (4), 577-594 (1979)
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Sequence analysis of adenovirus DNA.
Carboxy-terminal end of the gene for
Virology 91 (2), 477-480 (1978)
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Ziff,E.B. and Evans,R.M.
Coincidence of the promoter and capped adenovirus 2 major late transcription u Cell 15 (4), 1463-1475 (1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Akusjarvi,G. and Pettersson,U.

Nucleotide sequence at the junction between the coding region
the adenovirus 2 hexon messenger RNA and its leader sequence
Proc. Natl. Acad. Sci. U.S.A. 75 (12), 5822-5826 (1978)
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Studies of low molecular weight RNA from cells infected with adenovirus 2. II. Heterogeneity at the 5' end of VA-RNA I J. Biol. Chem. 252 (24), 9043-9046 (1977)
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MASTEAGENOVIRUS h5 gene, complete genome.

M73360.1 GI:209842
protein 5 precursor; protein IIIa; protein V; protein pVII; protein pVIII; brotein pVIII; protein bVIII; protein bVIII; protein bVIII; brotein bVIII; protein bVIII; protein bVIII; protein bVIII; protein bVIII; brotein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acgaccaacacgatetcggttgtctcggcgcactccgtacagtag 345
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Dedieu, J., Latta, W., Orsini, C., Perric CELLS FOR THE PRODUCTION OF RECOMBINAN Patent: WO 9622378-A 4 25-JUL-1996; RHONE POULENC ROKER SA (FR) Other publication AU 4544396 960807 Other publication FR 2729674 960726.
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FRQQPQANRLSAL LEAVVPARANPTHEKVLATVNALAENRA IRPEAGLYVPDALLQRV
ARXNSGNVOTHLDRLVGUVREAVAQRERAQQGLUSSWALIAAFLSTQPANVPRGQP
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PNNGLISLYDDKNSRWKTYAQDHRDVFGPRFTRPRLLGEEFYLNNSLLCAPCREKNLPPAF
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/protein_id="AAA96408.1"
/protein_id="AAA96408.1"
/db_xref="GI:209845"
/translation="MRAARRLAAGIVTVPPRSRRRAAAAAAAAISAMTQGRRGNVYWV
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/protein_id="AAA96407.1"
/db_xref="GI:289094"
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IVQHSRDNEAFRDALLNIVEPEGRWLLDLINILGSIVVQERSLSLADKVAAINVSMLS
IGKFYARKIYHTPYVPIDKEVKIEGFYMRMALKVLTLSDDLGVYRNERIHKAVSVSRR
RELSDRELMHSLQRALAGTGSGDREAESYFDAGADLRWAPSRRALEAAGAGPGLAVAP
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/db_xref-"taxon:28285"
<11565. .12297
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hes 345;
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ION Adenovirus type 2, complete genome.

J01917 J01918 J01919 J01920 J01921 J01922 J01923 J01924 J01925

DN J01916 J01927 J01928 J01929 J01930 J01931 J01932 J01933 J01934

J01935 J01936 J01937 J01938 J01939 J01940 J01940 J01943 J01934

J01935 J01936 J01937 J01938 J01939 J01940 J01950 J01951 J01932

J01934 J01945 J01955 J01956 J01957 K00086 K00394 K00395 K02367

M13004 V00007 V00008 V00009 V00011 V00012 V00013 V00014

V00015 V00016 V00017 V00018 V00019 V00020 V00023 V00024

J01917.1 GI:209811

DNA polymerase; DNA-binding protein; RNA polymerase III;

DNA polymerase; DNA-binding protein; complete genome; genome-linked protein; glycoprotein; overlapping genes; polymerase; terminal repeat; unidentified reading frame; virus-associated RNA.

Human adenovirus type 2.

ISM Human adenovirus type 2.
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         and Weissman, S.M.
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/KIRAHRURILLEQAAITTTPRUNLNPRSWPAALVYQESPAPTTVVLPRDAQAEVQMT
NSGAQLAGGERHRVRSPGQGITHLTIRGRGIQLUDESYSSSLGLRPDGTFQIGGAGRP
SETPRQAILTLQTSSSEPRSGGIGTLQFIEEFVPSVYFNPFSGPPGHYPDQFIPNFDA
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/protein_id="AAA96413.1"
/db_xref="GI:454806"
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Pred. No. 6.6e-97;
; Mismatches 0;
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J. Biol. Chem. 246 (22), 6991-7009 (1971)
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Akusjarvi.G. and Pettersson,U.
Sequence analysis of adenovirus DNA.
carboxy-terminal end of the gene for
Virology 91 (2), 477-480 (1978)
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Nucleotide sequence at the junction between the coding region
the adenovirus 2 hexon messenger RNA and its leader sequence
proc. Natl. Acad. Sci. U.S.A. 75 (12), 5822-5826 (1978)
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Characterization and sequence
the hybrid virus Ad2+ND
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5an, J., Celma, M.L. and Weissman, S.M.

5tudies of low molecular weight RNA from cells infected with adenovirus 2. III. The sequence of the promoter for VA-RNA I J. Biol. Chem. 252 (24), 9047-9054 (1977)
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21ff, E.B. and Evans, R.M.
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1 (bases 1 to 35935)
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The sequence of the genome of adenovirus type 5 and with the genome of adenovirus type 2
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RELSDRELMHSLORALAGTGSGDREAESYFDAGADLRWAPSRRALEAAGAGPGLAVAP
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RDGVTPSVALDMTARNMEPGMYASNRPFINRLMDYLHRAAAVNPEYFTNAILMPHWLS
RDGVTPSVALDMTARNMEPGMYASNRPFINRLMDYLHRAAAVNEEXPRPSS
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The nucleotide sequence of a low molecular from cells infected with adenovirus 2
J. Biol. Chem. 246 (22), 6991-7009 (1971)
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Sambrook, J., Roberts, R.J.,
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d N-terminus of adenovirus type 2 hexon protein
phys. Res. Commun. 56 (2), 304-310 (1974)
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ALHCHCSSPGSLQCIAGGQVLASWFRMYVDGAMFNQRFIWYREVVNYNMPKEVNFMSSVF

MRGRHLIYLRLWYDGHVGSVVPAMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCAR

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240 240

Query Match Best Local S Matches

Similarity

100.0%;

Score 1594; DB 1; Pred. No. 9.3e-142; Mismatches 0;

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294; 0

Gaps

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RESULT 2
\$10867 a 34K protein - human adenovirus 12
c:Species: Mastadenovirus h12 (human adenovirus 12)
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c:Species: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999
c:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999
c:Accession: \$10867; \$33952
c:Accession: \$10867; \$33952
R;Hogenkamp, T.; Esche, H.

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R;Herisse, J.; Rigolet, M.; Dupont de Dinechin, S.; Galibert, Nucleic Acids Res. 9, 4033-4042, 1981
Nucleic Nucleotide sequence of adenovirus 2 DNA fragment encc A;Reference number: A93733; MUID:82059444
A;Accession: A03805
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QAADC2

QAADC2

early E4 34K protein - human adenovirus 2

early E4 34K protein - human adenovirus 2)

C;Species: Mastadenovirus h2 (human adenovirus 2)

A;Note: host Homo sapiens (man)

A;Note: host Homo sapiens (man)

C;Date: 02-Apr-1982 *sequence_revision 02-Apr-1982 *text_change 04-Mar-1994

C;Date: 02-Apr-1982
A; Map position: 92.6-95.2
C; Superfamily: adenovirus
C; Keywords: early protein
                                   A; Note: this probable C; Genetics:
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